

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:19:12 ; Search time 12.3158 Seconds
(without alignments)
710.580 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539

Sequence: 1 KSPVVDGCHGDRSYRGIS.....DPCRWYCNLTQCSRTESG 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 539 | 100.0 | 4548 | 1 S00657 | apoprotein(a) (EC |
| 2 | 535 | 95.5 | 1420 | 2 A32869 | apolipoprotein(a) |
| 3 | 455 | 78.8 | 810 | 2 B30848 | plasma (EC 3.4.21 |
| 4 | 423 | 78.5 | 810 | 1 PLHU | plasma (EC 3.4.21 |
| 5 | 413 | 76.6 | 812 | 1 PLBO | plasma (EC 3.4.21 |
| 6 | 405 | 75.1 | 123 | 2 C61545 | plasma (EC 3.4.21 |
| 7 | 402 | 74.6 | 790 | 1 PLRG | plasma (EC 3.4.21 |
| 8 | 388 | 72.0 | 812 | 1 PLMS | plasma (EC 3.4.21 |
| 9 | 387 | 71.8 | 455 | 2 A61545 | plasma (EC 3.4.21 |
| 10 | 387 | 71.8 | 460 | 2 B61545 | plasma (EC 3.4.21 |
| 11 | 384 | 71.2 | 120 | 2 A61545 | plasma (EC 3.4.21 |
| 12 | 378 | 70.1 | 810 | 2 I46260 | plasma (EC 3.4.21 |
| 13 | 363.5 | 67.4 | 169 | 2 A40522 | plasma (EC 3.4.21 |
| 14 | 359 | 61.0 | 89 | 2 A60140 | plasma (EC 3.4.21 |
| 15 | 281 | 52.1 | 2869 | 2 T18518 | apolipoprotein(a) |
| 16 | 255 | 47.3 | 728 | 1 JH0579 | hepatocyte growth |
| 17 | 250.5 | 46.5 | 710 | 1 I51283 | hepatocyte growth |
| 18 | 250 | 46.4 | 728 | 1 A35644 | hepatocyte growth |
| 19 | 249.5 | 46.3 | 946 | 1 A47399 | hepatocyte growth |
| 20 | 249 | 46.2 | 728 | 1 A60185 | hepatocyte growth |
| 21 | 241.5 | 44.8 | 716 | 1 A40332 | macrophage-stimula |
| 22 | 238.5 | 44.2 | 716 | 1 JCS061 | macrophage-stimula |
| 23 | 232 | 43.0 | 411 | 2 I51285 | hepatocyte growth |
| 24 | 231.5 | 42.9 | 711 | 1 A47136 | macrophage-stimula |
| 25 | 204 | 37.8 | 336 | 2 S33879 | plasma precursor |
| 26 | 201.5 | 37.4 | 622 | 1 TBHU | chromin (EC 3.4.2 |
| 27 | 200.5 | 37.2 | 943 | 2 B45082 | neurotrophic recep |
| 28 | 200 | 37.1 | 617 | 2 S10511 | chromin (EC 3.4.2 |
| 29 | 196 | 36.4 | 618 | 2 A35827 | chromin (EC 3.4.2 |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 193.5 | 35.9 | 625 | 1 TBHO | thrombin (EC 3.4.2 |
| 31 | 190.5 | 35.3 | 560 | 1 JC4795 | plasma hyaluronan- |
| 32 | 189.5 | 35.2 | 937 | 2 A45082 | neurotrophic recep |
| 33 | 186 | 34.5 | 562 | 1 UKHTT | t-plasminogen acti |
| 34 | 181.5 | 33.7 | 603 | 2 S28941 | coagulation factor |
| 35 | 181.5 | 33.7 | 615 | 1 KFH12 | coagulation factor |
| 36 | 180.5 | 33.5 | 558 | 2 JCS878 | plasma hyaluronan- |
| 37 | 176.5 | 32.7 | 559 | 1 A35029 | t-plasminogen acti |
| 38 | 173.5 | 32.2 | 593 | 2 S45281 | coagulation factor |
| 39 | 173 | 32.1 | 559 | 1 A28941 | t-plasminogen acti |
| 40 | 173 | 32.1 | 655 | 1 A46688 | hepatocyte growth |
| 41 | 166 | 30.8 | 432 | 1 S18932 | u-plasminogen acti |
| 42 | 161 | 29.9 | 442 | 1 UKPG | u-plasminogen acti |
| 43 | 157 | 29.1 | 433 | 1 UKMS | u-plasminogen acti |
| 44 | 156 | 28.9 | 433 | 1 JN0560 | u-plasminogen acti |
| 45 | 148 | 27.5 | 433 | 1 UKRAY | u-plasminogen acti |

ALIGNMENTS

RESULT 1
S00657
apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N/Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 08-Dec-2000
C/Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
R/McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Bacon, D.L.; Chen, E.Y.; Fleiss, G.M.; Seam
Nature 330, 132-137, 1987
A/Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A/Reference number: S00657; MUID:88039109; PMID:3670400
A/Accession: S00657
A/Molecule type: mRNA
A/Residues: 1-4548 <MCL>
A/Cross-references: GB:X06290; EMBL:X06696; NID:928619; PIDN:CA29618.1; PID:928620
R/Bacon, D.L.; Fleiss, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.;
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A/Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to
A/Reference number: A28017; MUID:87204109; PMID:3472206
A/Accession: A28017
A/Molecule type: protein
A/Residues: 20-21, 'P', 23-34, 177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200;292-314, 'W', 316-318
X', 4396-4401 <EXT>
R/Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meier, K.; Schwartz, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A/Title: 5' control regions of the apolipoprotein(a) gene and members of the related pla
A/Reference number: A47277; MUID:93165698; PMID:7679504
A/Accession: A47277
A/Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-16 <RES>
A/Cross-references: GB:L07899; NID:9967973; PID:9967974
R/Margaret, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sacor
Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A/Title: Characterization by yeast artificial chromosome cloning of the linked apolipop
A/Reference number: A47233; MUID:93087573; PMID:1454851
A/Accession: A47233
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Residues: 1-16 <RES>
A/Molecule type: DNA
A/Cross-references: GB:M60078; NID:9178786; PIDN:AAA5547.1; PID:9553188
A/Note: apo(a) gene 1 (nomenclature of reference I52415)
A/Accession: A47233
A/Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-16 <RES>
A/Cross-references: GB:M60079; NID:9178784; PIDN:AAA5546.1; PID:9553187
R/Richmond, A.
Biochemistry 31, 3113-3118, 1992
A/Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated wit
A/Reference number: I52415; MUID:92207924; PMID:11554698
A/Accession: I52415

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 116 <RES>
 A/Cross-references: GB:M86877; NID:g178780; PIDN:AAA9909.1; PID:g553185
 A>Note: apo(a) gene 1 (nomenclature of reference 152415)
 A:Accession: 165286
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 116 <RES>
 A/Cross-references: GB:M86878; NID:g178782; PIDN:AAA51749.1; PID:g553186
 C:Genetic:
 A:Gene: GDB:LPA
 A/Cross-references: GDB:120699; OMIM:152200
 A:Map position: 6q26-6q27
 A>Note: several genes closely linked on chromosome 6 are identical in the first coding
 re of kringle repeats
 C/Superfamily: apolipoprotein(a); kringle homology; trypsin homology
 C/Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-4548/Product: apolipoprotein(a) #status experimental <MAT>
 F:28-105/Domain: kringle homology <KR1>
 F:142-219/Domain: kringle homology <KR2>
 F:256-333/Domain: kringle homology <KR3>
 F:370-447/Domain: kringle homology <KR4>
 F:484-561/Domain: kringle homology <KR5>
 F:598-675/Domain: kringle homology <KR6>
 F:712-789/Domain: kringle homology <KR7>
 F:826-903/Domain: kringle homology <KR8>
 F:940-1017/Domain: kringle homology <KR9>
 F:1054-1131/Domain: kringle homology <KR10>
 F:1168-1245/Domain: kringle homology <KR11>
 F:1282-1359/Domain: kringle homology <KR12>
 F:1396-1473/Domain: kringle homology <KR13>
 F:1510-1587/Domain: kringle homology <KR14>
 F:1624-1701/Domain: kringle homology <KR15>
 F:1738-1815/Domain: kringle homology <KR16>
 F:1852-1929/Domain: kringle homology <KR17>
 F:1965-2043/Domain: kringle homology <KR18>
 F:2080-2157/Domain: kringle homology <KR19>
 F:2194-2271/Domain: kringle homology <KR20>
 F:2308-2385/Domain: kringle homology <KR21>
 F:2422-2499/Domain: kringle homology <KR22>
 F:2536-2613/Domain: kringle homology <KR23>
 F:2650-2727/Domain: kringle homology <KR24>
 F:2764-2841/Domain: kringle homology <KR25>
 F:2878-2955/Domain: kringle homology <KR26>
 F:2992-3069/Domain: kringle homology <KR27>
 F:3106-3183/Domain: kringle homology <KR28>
 F:3220-3297/Domain: kringle homology <KR29>
 F:3334-3411/Domain: kringle homology <KR30>
 F:3448-3525/Domain: kringle homology <KR31>
 F:3562-3639/Domain: kringle homology <KR32>
 F:3676-3753/Domain: kringle homology <KR33>
 F:3782-3859/Domain: kringle homology <KR34>
 F:3896-3973/Domain: kringle homology <KR35>
 F:4010-4087/Domain: kringle homology <KR36>
 F:4124-4201/Domain: kringle homology <KR37>
 F:4228-4307/Domain: kringle homology <KR38>
 F:4328-4541/Domain: trypsin homology <TRY>
 Query Match 100.0%; Score 539; DB 1; Length 4548;
 Best Local Similarity 100.0%; Pred. No. 2, 4e-44;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KSPVVDCTHGDGRSYRGISSTVTGRTCSQSSMIPHHORTPENYPNAGLTENYCRNP 60
 DB 4003 KSPVVDCTHGDGRSYRGISSTVTGRTCSQSSMIPHHORTPENYPNAGLTENYCRNP 4062
 QY 61 DSGKQPCYTTDPCVRWEYCNLTQCSSTESG 91
 DB 4063 DSGKQPCYTTDPCVRWEYCNLTQCSSTESG 4093

RESULT 2
 A32869
 apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
 C/Species: Macaca mulatta (rhesus macaque)
 C/Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 22-Jun-1999
 C/Accession: A32869; A30848
 R/Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
 J. Biol. Chem. 264, 5957-5965, 1989
 A>Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
 A/Reference number: A32869; M01D:89174660; PMID:2925643
 A:Accession: A32869
 A:Molecule type: mRNA
 A:Residues: 1-1420 <TOM>
 A/Cross-references: GB:J04635; NID:g342072; PIDN:AAA6833.1; PID:g342073
 C/Superfamily: apolipoprotein(a); kringle homology; trypsin homology
 C/Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
 F:50-117/Domain: kringle homology <KR1>
 F:164-241/Domain: kringle homology <KR2>
 F:278-355/Domain: kringle homology <KR3>
 F:392-469/Domain: kringle homology <KR4>
 F:506-583/Domain: kringle homology <KR5>
 F:620-697/Domain: kringle homology <KR6>
 F:726-803/Domain: kringle homology <KR7>
 F:840-917/Domain: kringle homology <KR8>
 F:954-1031/Domain: kringle homology <KR9>
 F:1068-1145/Domain: kringle homology <KR10>
 F:1191-1413/Domain: trypsin homology <TRY>
 Query Match 95.5%; Score 515; DB 2; Length 1420;
 Best Local Similarity 94.5%; Pred. No. 1, 8e-42;
 Matches 86; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KSPVVDCTHGDGRSYRGISSTVTGRTCSQSSMIPHHORTPENYPNAGLTENYCRNP 60
 DB 947 KSPVVDCTHGDGRSYRGISSTVTGRTCSQSSMIPHHORTPENYPNAGLTENYCRNP 1006
 QY 61 DSGKQPCYTTDPCVRWEYCNLTQCSSTESG 91
 DB 1007 DSGKQPCYTTDPCVRWEYCNLTQCSSTESG 1037
 RESULT 3
 B30848
 plasmin (EC 3.4.21.7) precursor - rhesus macaque
 C/Species: Macaca mulatta (rhesus macaque)
 C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
 C/Accession: B32869; B30848
 R/Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
 J. Biol. Chem. 264, 5957-5965, 1989
 A>Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
 A/Reference number: A32869; M01D:89174660; PMID:2925643
 A:Accession: B32869
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-810 <TOM>
 A/Cross-references: GB:J04697; NID:g342272; PIDN:AAA6901.1; PID:g342273
 C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-96/Domain: signal sequence #status predicted <SIG>
 F:103-181/Domain: kringle homology <KR1>
 F:185-262/Domain: kringle homology <KR2>
 F:275-352/Domain: kringle homology <KR3>
 F:377-454/Domain: kringle homology <KR4>
 F:481-560/Domain: kringle homology <KR5>
 F:581-603/Domain: trypsin homology <TRY>
 F:49-73, 53-61, 103-181, 124-164, 152-176, 185-262, 188-316, 206-245, 234-257, 275-352, 296-335, 324-
 bonds: #status predicted
 F:622, 665, 760/Active site: His, Asp, Ser #status predicted
 Query Match 78.8%; Score 425; DB 2; Length 810;
 Best Local Similarity 77.3%; Pred. No. 6, 7e-34;
 Matches 68; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

[illegible]

A:Title: J. Biochem. 76, 129-137, 1977
 A:Title: Primary structure of the B-chain of human plasmin.
 A:Reference number: A04627; MUID:77225245; PMID:142009
 A:Accession: A04627
 A:Molecule type: protein
 A:Residues: 581-810 <W11>
 R:Wiman, B.; Wallen, P.
 Eur. J. Biochem. 50, 489-494, 1975
 A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen.
 A:Reference number: A04625; MUID:75093329; PMID:122932
 A:Accession: A04625
 A:Molecule type: protein
 A:Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <W12>
 R:Wiman, B.; Wallen, P.
 Eur. J. Biochem. 58, 539-547, 1975
 A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen that contains the primary structure of the B-chain.
 A:Reference number: A04626; MUID:76043692; PMID:126863
 A:Accession: A04626
 A:Molecule type: protein
 A:Residues: 483-507, 'E', 509-604 <W13>
 R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
 J. Biol. Chem. 248, 1631-1633, 1973
 A:Title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen.
 A:Reference number: A92125; MUID:73149248; PMID:4694729
 A:Contents: annotation; active site
 R:Groskopf, W.R.; Summaria, L.; Robbins, K.C.
 J. Biol. Chem. 244, 3590-3597, 1969
 A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a plasminogen fragment containing the active site.
 A:Reference number: A92048; MUID:69234739; PMID:4240117
 A:Contents: annotation; active site
 R:Rexler, M.; Vail, Z.; Patchy, L.
 J. Biol. Chem. 257, 7401-7406, 1982
 A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
 A:Reference number: A92382; MUID:82213905; PMID:6919539
 A:Contents: annotation; omega-aminocarboxylic acid binding sites
 R:Vali, Z.; Patchy, L.
 J. Biol. Chem. 259, 13690-13694, 1984
 A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential for fibrin binding.
 A:Reference number: A92458; MUID:85054794; PMID:6094526
 A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
 R:Geo, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehnel, S.; Mccance, S.G.; J. Biol. Chem. 271, 29461-29467, 1996
 A:Title: Kring domains of human angiotensin. Characterization of the anti-proliferative activity of the kring domain.
 A:Reference number: A58811; MUID:97067211; PMID:8910613
 A:Contents: annotation
 R:Lijnen, H.R.; Uegwi, F.; Bini, A.; Collen, D.
 Biochemistry 37, 4699-4702, 1998
 A:Title: Generation of an angiotensin-like fragment from plasminogen by streptolysin-1 (M13).
 A:Reference number: A58812; MUID:9548753; PMID:9548753
 A:Contents: annotation
 R:Tulinaky, A.; Mlichnak, A.M.
 submitted to the Brookhaven Protein Data Bank, July 1991
 A:Reference number: A51341; PDB:1PK4
 A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
 R:Tulinaky, A.; Wu, T.P.
 submitted to the Brookhaven Protein Data Bank, July 1991
 A:Reference number: A51488; PDB:2PK4
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
 R:Wu, T.P.; Tulinaky, A.
 submitted to the Brookhaven Protein Data Bank, August 1993
 A:Reference number: A51911; PDB:1PKR
 A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
 R:Padmanabhan, K.; Tulinaky, A.
 submitted to the Brookhaven Protein Data Bank, April 1994
 A:Reference number: A52408; PDB:1PKK
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
 R:Tulinaky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995
 A:Reference number: A65244; PDB:1CEA
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
 R:Tulinaky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995

A:Reference number: A65245; PDB:1CEB
 A:Contents: annotation: X-ray crystallography, 2.1 angstroms, residues 102-181
 R:Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
 Biochemistry 30, 10576-10588, 1991
 A:Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 Å
 A:Reference number: A58919; PMID:92031502; PMID:1657148
 A:Contents: annotation
 R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
 Biochemistry 30, 10589-10594, 1991
 A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin
 A:Reference number: A58818; PMID:92031503; PMID:1657149
 A:Contents: annotation
 R:de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.
 Biochemistry 31, 270-279, 1992
 A:Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.0 Å
 A:Reference number: A39483; PMID:92118803; PMID:1310033
 A:Contents: annotation: X-ray crystallography, 2.4 angstroms
 R:Stec, B.; Teeler, M.M.; Whitlow, M.; Yamano, A.
 submitted to the Brookhaven Protein Data Bank, June 1995
 A:Reference number: A65980; PDB:1KRN
 A:Contents: annotation: X-ray crystallography, 1.67 angstroms, residues 376-454
 R:Rejzante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A65803; PDB:1HPJ
 A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
 R:Rejzante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A65804; PDB:1HPK
 A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
 R:Rejzante, M.R.; Llinas, M.
 Eur. J. Biochem. 221, 927-937, 1994
 A:Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
 A:Reference number: S43545; PMID:94237157; PMID:8181475
 A:Contents: annotation: conformation by (1)H-NMR, residues 96-184
 R:Rejzante, M.R.; Llinas, M.
 Eur. J. Biochem. 221, 939-949, 1994
 A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
 A:Reference number: A58817; PMID:94237158; PMID:8181476
 A:Contents: annotation: conformation by (1)H-NMR
 A:Comment: plasminogen is synthesized by the kidney and is present in plasma and many of
 C:Comment: plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU a
 d PIR:FGHUGB).
 C:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITPNUA2) immediately af
 rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor,
 C:Comment: Microplasmin is formed by autocatalytic cleavage of plasmin under artificial cond
 C:Comment: Streptolysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiotensin. Th
 cing solid tumors.
 C:Genetics:
 A:Gene: GDB:PLG
 A:Cross-references: GDB:119498; OMIM:173350
 A:Map position: 6q26-6q27
 A:Features: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 528
 A:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 as the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
 F:1-19/Domains: signal sequence #status predicted <SIG>
 F:20-810/Product: plasminogen #status predicted <PRO>
 F:20-96/Domains: activation peptide #status experimental <APT>
 F:79-466/Product: angiotensin #status experimental <AS>
 F:97-580,581-810/Product: plasmin #status experimental <AMT>
 F:97-580,581-810/Product: plasmin chain A #status experimental <CHA>
 F:103-181/Domains: kringle homology <KR1>
 F:185-262/Domains: kringle homology <KR2>
 F:275-352/Domains: kringle homology <KR3>
 F:377-454/Domains: kringle homology <KR4>
 F:481-560/Domains: kringle homology <KR5>
 F:550-580,581-810/Product: microplasmin #status experimental <MPT>

Query Match 78.5%; Score 423; DB 1; Length 810;

Best Local Similarity 78.7%; Pred. No. 16-33;
 Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 Oy 2 SPVPOOCYCHGDDRSYVIGSSTTYTGTCOSWSMT PHHQRTPENYPMAGLTENYCRND 61
 Db 371 TPVPOQCHYGDQOSTKRGTSITTTGKKCCOSWSMTPHRQKTPENYPMAGLTENYCRND 430
 Oy 62 SGKQPCYTTDPCVREWCNLTQCSSETS 90
 Db 431 ADKGPCFTTDPSTVREWCNLTQCSSETS 459
 RESULT 5
 P1BO
 Plasmin (EC 3.4.21.7) Precursor - bovine
 N/Alternate names: plasminogen
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 30-Sep-1987 #sequence, revision 28-Apr-1995 #text_change 18-Jun-1999
 C/Accession: S45046; A25835; I45961; S03736
 R/Berglund, L.; Andersen, M.D.; Petersen, T.E.
 submitted to the EMBL Data Library, May 1994
 A:Description: Cloning and characterization of the bovine plasminogen cDNA.
 A:Reference number: S45046
 A:Accession: S45046
 A:Molecule type: mRNA
 A:Residues: 1-812 <BER>
 A:Cross-references: EMBL:X79402; NID:g494962; PIDN:CAAS5939.1; PID:g494963
 A:Experimental source: liver
 A:Note: It is uncertain whether Met-1 or Met-8 is the initiator
 R/Schaller, J.; Moser, P.W.; Danneberg-Muller, G.A.K.; Kosseler, S.J.; Kamfer, U.; Rick
 Eur. J. Biochem. 149, 267-278, 1985
 A:Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasmi
 A:Reference number: A25835; PMID:85203906; PMID:3846532
 A:Accession: A25835
 A:Molecule type: protein
 A:Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
 R/Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
 Biochemistry 23, 4243-4250, 1984
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and l
 A:Reference number: I45961; PMID:85023311; PMID:6148961
 A:Accession: I45961
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 706-743, 'R', 745-812 <MAL>
 A:Cross-references: GB:K02935; NID:g163551; PIDN:AAA0714.1; PID:g163552
 R/Brunsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
 Eur. J. Biochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human, l
 A:Reference number: S03735; PMID:81212097; PMID:7238497
 A:Accession: S03736
 A:Molecule type: protein
 A:Residues: 27-83 <BRU>
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 as the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;
 F:1-26/Domains: signal sequence #status predicted <SIG>
 F:27-103/Domains: plasminogen-related protein precursor homology <PLPH>
 F:27-103/Product: plasminogen #status experimental <PRO>
 F:104-583,584-812/Product: plasmin #status experimental <AMT>
 F:104-583,584-812/Product: plasmin chain A #status experimental <ACH>
 F:110-583/Domains: plasmin chain A #status experimental <ACH>
 F:110-188/Domains: kringle homology <KR1>
 F:192-269/Domains: kringle homology <KR2>
 F:282-359/Domains: kringle homology <KR3>
 F:384-461/Domains: kringle homology <KR4>
 F:485-564/Domains: kringle homology <KR5>
 F:584-812/Domains: plasmin chain B #status experimental <BCH>
 F:584-805/Domains: trypsin homology <TRY>
 F:56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,331
 bonds: #status predicted

as the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
 F:1-96/Domain: plasminogen-related protein precursor homology <PLP>
 F:1-19/Domain: plasmin sequence #status predicted <SIG>
 F:20-812/Product: plasminogen #status predicted <PRO>
 F:20-96/Domain: activation peptide #status predicted <APT>
 F:79-466/Product: angiotensin #status predicted <AST>
 F:97-581,582-812/Product: plasmin #status predicted <MAT>
 F:97-581/Domain: chain A #status predicted <ACH>
 F:103-181/Domain: kringle homology <KR1>
 F:185-262/Domain: kringle homology <KR2>
 F:275-352/Domain: kringle homology <KR3>
 F:377-454/Domain: kringle homology <KR4>
 F:481-560/Domain: kringle homology <KR5>
 F:582-812/Domain: chain B #status predicted <BCH>
 F:582-805/Domain: trypsin homology <TRY>
 F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
 F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
 F:136,308/Cleavage site: carboxylate (Asn) (covalent) #status predicted
 F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
 F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
 F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 72.0%; Score 388; DB 1; Length 812;
 Best Local Similarity 70.5%; Pred. No. 2.8e-30; Indels 0; Gaps 0;
 Matches 62; Conservative 12; Mismatches 14;

Qy 1 KSPVDDCHGDRSRYSISSTVTGRTCSQSSMIPMHQRPENYPNAGLTENYCRNP 60
 Db 370 QTVVDECVCSDDQSYRGTSSTITIGKKCSWAMFHRSKTPEPNPDAGLEMYCRNP 429

Qy 61 DSGKQPCVCTTDPCEVMEYCNLTQCSSET 88
 Db 430 DGDGKPCVCTTDPSEVMEYCNLTQCSSET 457

RESULT 9

A61545
 plasmin (BC 3.4.21.7) precursor - horse (fragments)
 N:Alternate names: plasminogen
 N:Contains: miniplasminogen
 C:Species: Equus caballus (domestic horse)
 C>Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
 C/Accession: A61545; S17527
 R:Schaller, J.; Rickli, E.E.
 Enzyme 40, 63-69, 1988
 A>Title: Structural aspects of the plasminogen of various species.
 A:Reference number: A61545; PMID:89005015; PMID:3168975
 A/Accession: A61545
 A:Molecule type: protein
 A:Residues: 1-33,34-117 <SCH>
 R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
 Protein Seq. Data Anal. 4, 69-74, 1991
 A>Title: Complete amino acid sequence of equine miniplasminogen.
 A:Reference number: S17527; PMID:9205077; PMID:1946332
 A/Accession: S17527
 A:Molecule type: protein
 A:Residues: 118-455 <SC2>
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z
 F:1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <PRO>
 F:1-33/Domain: activation peptide (fragment) #status experimental <APT>
 F:34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <MAT>
 F:37-114/Domain: kringle homology <KR4>
 F:118-455/Product: miniplasminogen #status experimental <MIN>
 F:126-205/Domain: kringle homology <KR5>
 F:226-455/Domain: plasmin chain B #status experimental <BCH>
 F:226-448/Domain: trypsin homology <TRY>
 F:267,310,405/Active site: His, Asp, Ser #status predicted

Query Match 71.8%; Score 387; DB 2; Length 455;
 Best Local Similarity 76.2%; Pred. No. 2e-30;
 Matches 64; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 5 VDDCHGDRSRYSISSTVTGRTCSQSSMIPMHQRPENYPNAGLTENYCRNPDSK 64
 Db 34 VDDCVDDKESYRGTSSTVTGRTCSQSSMIPMHQRPENYDNLTYNCRNPDSK 93

Qy 65 QPCVCTTDPCEVMEYCNLTQCSSET 88
 Db 94 GPCVCTTDPSEVMEYCNLTQCSSET 117

RESULT 10

B61545
 plasmin (BC 3.4.21.7) precursor - sheep (fragments)
 N:Alternate names: plasminogen
 N:Contains: miniplasminogen
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C>Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999
 C/Accession: B61545; S28200
 R:Schaller, J.; Rickli, E.E.
 Enzyme 40, 63-69, 1988
 A>Title: Structural aspects of the plasminogen of various species.
 A:Reference number: A61545; PMID:89005015; PMID:3168975
 A/Accession: B61545
 A:Molecule type: protein
 A:Residues: 1-37,38-117 <SCH>
 R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
 Protein Seq. Data Anal. 5, 21-25, 1992
 A>Title: Complete amino acid sequence of ovine miniplasminogen.
 A:Reference number: S28200; PMID:93149995; PMID:1492092
 A/Accession: S28200
 A:Molecule type: protein
 A:Residues: 118-460 <SC2>

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z
 F:1-37,38-117,118-460/Product: plasminogen (fragments) #status experimental <PRO>
 F:1-37/Domain: activation peptide (fragment) #status experimental <APT>
 F:38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT>
 F:41-118/Domain: kringle homology <KR4>
 F:118-460/Product: miniplasminogen #status experimental <MIN>
 F:132-211/Domain: kringle homology <KR5>
 F:226-460/Domain: plasmin chain B #status experimental <BCH>
 F:231-453/Domain: trypsin homology <TRY>
 F:272,315,410/Active site: His, Asp, Ser #status predicted

Query Match 71.8%; Score 387; DB 2; Length 460;
 Best Local Similarity 75.3%; Pred. No. 2e-30;
 Matches 64; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 6 ODCYHDDGRSRYSISSTVTGRTCSQSSMIPMHQRPENYPNAGLTENYCRNPDSKQ 65
 Db 39 ODCYHDDGRSRYSISSTVTGRTCSQSSMIPMHQRPENYDNLTYNCRNPDSK 98

Qy 66 PWCYCTTDPCEVMEYCNLTQCSSET 90
 Db 99 PWCYCTTDPSEVMEYCNLTQCSSET 123

RESULT 11

E61545
 plasmin (BC 3.4.21.7) precursor - dog (fragments)
 N:Alternate names: plasminogen
 C:Species: Canis lupus familiaris (dog)
 C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
 C/Accession: E61545
 R:Schaller, J.; Rickli, E.E.
 Enzyme 40, 63-69, 1988
 A>Title: Structural aspects of the plasminogen of various species.
 A:Reference number: A61545; PMID:89005015; PMID:3168975
 A/Accession: E61545
 A>Status: preliminary

A:Molecule type: protein
A:Residues: 1-120 <SCH>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: hydrolase; serine proteinase
F:37-114/Domain: kringle homology <KR4>

Query Match 71.2%; Score 384; DB 2; Length 120;
Best Local Similarity 70.9%; Pred. No. 1.1e-30;
Matches 61; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 5 VDDCTGDDGSRYSRISSTVTGRTCSQSSMIPMHQRTPEYVNAAGLTENYCRNP 64
DB 34 VDECTGDDGSRYSRISSTVTGRTCSQSSMIPMHQRTPEYVNAAGLTENYCRNP 93

QY 65 QPVCYTTPDCVRWEYCNLTQCSSETS 90
DB 94 SPWCYTTPDPSVRWEYCNLTQCSSETS 119

RESULT 12

146260 plasmin (EC 3.4.21.7) precursor - western European hedgehog
C:Species: Erinaceus europaeus (western European hedgehog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: 146260

R:Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong, J. Biol. Chem. 270, 24004-24009, 1995
A>Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein A:Reference number: 146259; MUID:96025778; PMID:7592597

A:Accession: 146260
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-810 <LAW>
A:Cross-references: EMBL:U33171, NID:g1046360, PID:g1046361
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology

C:Keywords: hydrolase; serine proteinase
F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F:103-181/Domain: kringle homology <KR1>
F:185-262/Domain: kringle homology <KR2>
F:275-352/Domain: kringle homology <KR3>
F:379-456/Domain: kringle homology <KR4>
F:482-561/Domain: kringle homology <KR5>
F:582-803/Domain: trypsin homology <TRY>

Query Match 70.1%; Score 378; DB 2; Length 810;
Best Local Similarity 68.5%; Pred. No. 2.6e-29;
Matches 61; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 KSPVDDCTGDDGSRYSRISSTVTGRTCSQSSMIPMHQRTPEYVNAAGLTENYCRNP 60
DB 372 QPVCYTTPDCVRWEYCNLTQCSSETS 431

QY 61 DSGKQPCVYTTPDCVRWEYCNLTQCSSETS 89
DB 432 DGDGKPCVYTTPDCVRWEYCNLTQCSSETS 460

RESULT 13

A40522 plasmin (EC 3.4.21.7) precursor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C:Accession: A40522

R:Kanaiah, U.J.; Makker, S.P.
J. Biol. Chem. 266, 10825-10829, 1991
A>Title: Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor for plasminogen: A40522, MUID:91250378; PMID:1645711

A:Accession: A40522
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-169 <KAN>
A:Cross-references: GB:M62832, NID:g206215, PIDN:AAA1884.1, PID:g554488

A>Note: the authors translated the codon TCT for residue 76 as Ala

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:34-112/Domain: kringle homology <KR3>
F:34-112,55-95,83-107/Disulfide bonds: #status predicted

Query Match 67.4%; Score 363.5; DB 2; Length 169;
Best Local Similarity 65.2%; Pred. No. 1.5e-28;
Matches 60; Conservative 15; Mismatches 16; Indels 1; Gaps 1;

QY 1 KSPVDDCTGDDGSRYSRISSTVTGRTCSQSSMIPMHQRTPEYVNAAGLTENYCRNP 60
DB 27 QPVCYTTPDCVRWEYCNLTQCSSETS 86

QY 61 DSGKQPCVYTTPDCVRWEYCNLTQCSSETS 91
DB 87 DNDGKPCVYTTPDCVRWEYCNLTQCSSETS 118

RESULT 14

A60140 plasmin (EC 3.4.21.7) precursor - chicken (fragment)
N:Alternate names: plasminogen
C:Species: Gallus gallus (chicken)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
C:Accession: A60140

R:Gyenes, M.; Patchy, L.
Biochim. Biophys. Acta 832, 326-330, 1985
A>Title: The kringle 4 domain of chicken plasminogen.
A:Reference number: A60140; MUID:86077796; PMID:4074753

A:Accession: A60140
A:Status: preliminary
A:Molecule type: protein

A:Residues: 1-89 <GYE>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
F:6-83/Domain: kringle homology <KR3>
F:6-83,27-66,55-78/Disulfide bonds: #status predicted

F:6-83/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 61.0%; Score 329; DB 2; Length 89;
Best Local Similarity 61.0%; Pred. No. 2e-25;
Matches 50; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 6 ODCYGDGSRYSRISSTVTGRTCSQSSMIPMHQRTPEYVNAAGLTENYCRNP 65
DB 4 EBCYGDGSRYSRISSTVTGRTCSQSSMIPMHQRTPEYVNAAGLTENYCRNP 63

QY 66 PWCYTTPDCVRWEYCNLTQCSSETS 87
DB 64 PWCYTTPDCVRWEYCNLTQCSSETS 85

RESULT 15

T18518 apolipoprotein(a) - western European hedgehog (fragment)
C:Species: Erinaceus europaeus (western European hedgehog)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C:Accession: T18518

R:Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong, J. Biol. Chem. 270, 24004-24009, 1995
A>Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein A:Reference number: 146259; MUID:96025778; PMID:7592597

A:Accession: T18518
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2869 <LAW>
A:Cross-references: EMBL:U33170, NID:g1046358, PID:g1046359, PIDN:AA40522.1

A:Experimental source: liver
A:Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, contains apolipoprotein(a).

Query Match 52.1%; Score 281; DB 2; Length 2869;
Best Local Similarity 51.7%; Pred. No. 2.7e-19;
Matches 45; Conservative 8; Mismatches 34; Indels 0; Gaps 0;

| | | | | | | |
|----|------|--|--------------|-----------|--------|----|
| Qy | 4 | VVODCYHGDGRSYRGISSTVTGRTGTCOSWSSMI | PHWHQRTPEPNY | PNAGLTENY | CRNPDG | 63 |
| Db | 2680 | IPDOCLEGTGENTRGSAVATVSGHTCORMRQSPHSHSRTPENYPTNLFENYCRNPDGE | 2739 | | | |
| Qy | 64 | KOPWCYTTDPQVRWEYCNLTCSETES | 90 | | | |
| Db | 2740 | VAPWCYTTNSAVRWEYCKIPSCNSSS | 2766 | | | |

Search completed: January 12, 2004, 17:26:23
 Job time : 12.3158 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:17:22 ; Search time 7.86842 Seconds

(without alignments)
543.874 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539

Sequence: 1 KSPVQDCHGDDGRSYRGIS.....DPCVMEXCNLTQCSSETS6G 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt 41.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 539 | 100.0 | 4548 | 1 | APOA_HUMAN |
| 2 | 515 | 95.5 | 1420 | 1 | APOA_MACMU |
| 3 | 425 | 78.8 | 810 | 1 | PLMN_MACMU |
| 4 | 423 | 78.5 | 810 | 1 | PLMN_HUMAN |
| 5 | 413 | 76.6 | 812 | 1 | PLMN_BOVIN |
| 6 | 402 | 74.6 | 790 | 1 | PLMN_PIG |
| 7 | 388 | 72.0 | 812 | 1 | PLMN_MOUSE |
| 8 | 378 | 70.1 | 810 | 1 | PLMN_ERIEU |
| 9 | 363.5 | 67.4 | 169 | 1 | HGF_HUMAN |
| 10 | 255 | 47.3 | 728 | 1 | HGF_HUMAN |
| 11 | 250 | 46.4 | 728 | 1 | HGF_RAT |
| 12 | 249 | 46.2 | 728 | 1 | HGF_MOUSE |
| 13 | 241.5 | 44.8 | 716 | 1 | HGFL_MOUSE |
| 14 | 236 | 43.8 | 343 | 1 | PLMN_SHEEP |
| 15 | 231.5 | 42.9 | 711 | 1 | HGFL_HUMAN |
| 16 | 226 | 41.9 | 333 | 1 | PLMN_CANFA |
| 17 | 222 | 41.2 | 338 | 1 | PLMN_HORSE |
| 18 | 204 | 37.8 | 325 | 1 | PLMN_PETMA |
| 19 | 201.5 | 37.4 | 622 | 1 | THRB_HUMAN |
| 20 | 200.5 | 37.2 | 943 | 1 | ROR2_HUMAN |
| 21 | 200 | 37.1 | 617 | 1 | THRB_RAT |
| 22 | 196 | 36.4 | 618 | 1 | THRB_MOUSE |
| 23 | 195.5 | 36.3 | 944 | 1 | ROR2_MOUSE |
| 24 | 193.5 | 35.9 | 625 | 1 | THRB_BOVIN |
| 25 | 193.5 | 35.9 | 724 | 1 | ROR2_DROME |
| 26 | 190.5 | 35.3 | 937 | 1 | ROR1_MOUSE |
| 27 | 189.5 | 35.2 | 937 | 1 | ROR1_HUMAN |
| 28 | 186 | 34.5 | 562 | 1 | TPA_HUMAN |
| 29 | 181.5 | 33.7 | 603 | 1 | FAI2_CAVPO |
| 30 | 181.5 | 33.7 | 615 | 1 | FAI2_HUMAN |
| 31 | 181 | 33.6 | 565 | 1 | TPA_BOVIN |
| 32 | 177 | 32.8 | 553 | 1 | HGFA_MOUSE |
| 33 | 176.5 | 32.7 | 559 | 1 | TPA_RAT |

| | | | | | | |
|----|-------|------|-----|---|-------------|---------------------|
| 34 | 173.5 | 32.2 | 593 | 1 | FAI2_BOVIN | P98140 bos taurus |
| 35 | 173 | 32.1 | 655 | 1 | HGFA_HUMAN | Q04756 homo sapien |
| 36 | 172 | 31.9 | 559 | 1 | TPA_MOUSE | P11214 mus musculus |
| 37 | 166 | 30.8 | 432 | 1 | UROK_RAT | P29598 rattus norv |
| 38 | 163 | 30.2 | 462 | 1 | KRM2_HUMAN | Q88C00 homo sapien |
| 39 | 161.5 | 30.0 | 473 | 1 | KRM1_MOUSE | Q99N43 mus musculus |
| 40 | 161.5 | 30.0 | 473 | 1 | KRM1_RAT | Q92484 rattus norv |
| 41 | 161 | 29.9 | 442 | 1 | UROK_PIG | P04185 sus scrofa |
| 42 | 158.5 | 29.4 | 475 | 1 | KRM1_HUMAN | Q96M08 homo sapien |
| 43 | 158 | 29.3 | 461 | 1 | KRM2_MOUSE | Q8K187 mus musculus |
| 44 | 157.5 | 29.2 | 452 | 1 | KRM1_XENTLA | Q90Y90 xenopus lae |
| 45 | 157 | 29.1 | 433 | 1 | UROK_MOUSE | P06869 mus musculus |

ALIGNMENTS

RESULT 1
APOA_HUMAN STANDARD; PRT; 4548 AA.
AC P08519;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Irp(a)).
GN LPA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=88039109; PubMed=3570400;
RX MEDLINE=90076123; PubMed=2531657;
RA Salonen E.-M., Jauhainen M., Zardi L., Vaheri A., Ehnholm C.;
RT "Lipoprotein(a) binds to fibronectin and has serine proteinase
RT activity capable of cleaving it.";
RL EMO J. 8:4035-4040(1989).
RN [3]
RP REVIEW.
RX MEDLINE=90049223; PubMed=2530631;
RA Utermann G.;
RT "The mysteries of lipoprotein(a).";
RL Science 246:904-910(1989).
RN [4]
RP CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
RX MEDLINE=21303595; PubMed=11294842;
RA Garner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.;
RT "Structural elucidation of the N- and O-glycans in concurring protease
RT resistance.";
RL J. Biol. Chem. 276:22200-22208(2001).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
RX MEDLINE=96217891; PubMed=8642595;
RA Mikol V., Lograsse P.V., Boettcher B.R.;
RT "Crystal structures of apolipoprotein(a) kringle IV37 free and
RT complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic
RT acid: existence of novel and expected binding modes.";
RL J. Mol. Biol. 256:751-761(1996).
RN [6]
RP VARIANT ARG-4193.
RX MEDLINE=95002201; PubMed=7918682;
RA Scannu A.M., Pfaffinger D., Lee J.C., Himman J.;
RT "A single point mutation (Trp72->Arg) in human apo(a) kringle 4-37
RT associated with a lysine binding defect in Lp(a).";

RL Blochim. Biophys. Acta 1227:41-45(1994).
 CC -1- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
 CC (Lp(a)). It has serine proteinase activity and is able of
 CC autoproteolysis. Inhibits tissue-type plasminogen activator 1.
 CC Lp(a) may be a ligand for megalin/Gp 330.
 CC -1- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibrinectin and
 CC decorin.
 CC -1- PTM: N- and O-glycosylated. The N-glycans are complex biantennary
 CC structures present in either a mono- or disialylated state. The
 CC O-glycans are mostly (80%) represented by the monosialylated core
 CC type I structure, NeuAcalpha2-3Galbeta1-3GalNAc, with smaller
 CC amounts of disialylated and non-sialylated O-glycans also
 CC detected.
 CC -1- DISEASE: Elevated plasma concentrations of apo(a) and its
 CC naturally occurring proteolytic fragments are correlated with
 CC atherosclerosis. Homology with plasminogen kringle IV and V is
 CC thought to underlie the atherogenicity of the protein, because the
 CC fragments are competing with plasminogen for fibrinogen binding.
 CC MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
 CC leading to the formation of the so called mini-Lp(a). Apo(a)
 CC fragments accumulate in atherosclerotic lesions, where they may
 CC promote thrombogenesis. O-glycosylation may limit the extent of
 CC proteolytic fragmentation.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 38 kringle domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL: X06290; CAA29618.1; -.
 CC PIR: S00657; S00657.
 CC PDB: 1I71; 13-JUN-01.
 CC PDB: 1JFM; 28-JUN-02.
 CC PDB: 1KIV; 18-MAY-99.
 CC PDB: 3KIV; 18-MAY-99.
 CC PDB: 4KIV; 18-MAY-99.
 CC MEROPS: S01.226; -.
 CC Gene: HGNC:6667; LPA.
 CC MIM: 152200; -.
 CC GO: GO:000466; F: endopeptidase inhibitor activity; TAS.
 CC GO: GO:0008015; P: circulation; TAS.
 CC GO: GO:0009405; P: pathogenesis; TAS.
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR001254; Ser protease_Try.
 CC Pfam: PF00051; kringle; 38.
 CC Pfam: PF00089; trypsin; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00018; KRINGLE.
 CC ProDom: PD000395; Kringle; 38.
 CC SMART: SM00130; KR: 38.
 CC SMART: SM00020; TRYP_SPC; 1.
 CC PROSITE: PS00021; KRINGLE_1; 38.
 CC PROSITE: PS00070; KRINGLE_2; 38.
 CC PROSITE: PS50240; TRYPsin DOM; 1.
 CC PROSITE: PS00134; TRYPsin HIS; 1.
 CC PROSITE: PS00135; TRYPsin SER; 1.
 CC HydroLase: Serine protease; Lipid transport; Plasma; Glycoprotein;
 CC Kringle; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure.
 CC KW HydroLase; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure.
 CC FT STGNL 1 19
 CC FT CHAIN 20 4548 APOLIPOPROTEIN(A).
 CC FT DOMAIN 20 130 KRINGLE TYPE IV, 1.
 CC FT DOMAIN 131 244 KRINGLE TYPE IV, 2.
 CC FT DOMAIN 245 358 KRINGLE TYPE IV, 3.
 CC FT DOMAIN 359 472 KRINGLE TYPE IV, 4.
 CC FT DOMAIN 473 586 KRINGLE TYPE IV, 5.
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 FT ACT_SITE 45153 45266 CHARGE RELAY SYSTEM.
 FT ACT_SITE 45267 45380 CHARGE RELAY SYSTEM.
 FT ACT_SITE 45381 45494 CHARGE RELAY SYSTEM.
 FT ACT_SITE 45495 45608 CHARGE RELAY SYSTEM.
 FT ACT_SITE 45609 45722 CHARGE RELAY SYSTEM.
 FT ACT_SITE 45723 45836 CHARGE RELAY SYSTEM.
 FT ACT_SITE 45837 45950 CHARGE RELAY SYSTEM.
 FT ACT_SITE 45951 46064 CHARGE RELAY SYSTEM.
 FT ACT_SITE 46065 46178 CHARGE RELAY SYSTEM.
 FT ACT_SITE 46179 46292 CHARGE RELAY SYSTEM.
 FT ACT_SITE 46293 46406 CHARGE RELAY SYSTEM.
 FT ACT_SITE 46407 46520 CHARGE RELAY SYSTEM.
 FT ACT_SITE 46521 46634 CHARGE RELAY SYSTEM.
 FT ACT_SITE 46635 46748 CHARGE RELAY SYSTEM.
 FT ACT_SITE 46749 46862 CHARGE RELAY SYSTEM.
 FT ACT_SITE 46863 46976 CHARGE RELAY SYSTEM.
 FT ACT_SITE 46977 47090 CHARGE RELAY SYSTEM.
 FT ACT_SITE 47091 47204 CHARGE RELAY SYSTEM.
 FT ACT_SITE 47205 47318 CHARGE RELAY SYSTEM.
 FT ACT_SITE 47319 47432 CHARGE RELAY SYSTEM.
 FT ACT_SITE 47433 47546 CHARGE RELAY SYSTEM.
 FT ACT_SITE 47547 47660 CHARGE RELAY SYSTEM.
 FT ACT_SITE 47661 47774 CHARGE RELAY SYSTEM.
 FT ACT_SITE 47775 47888 CHARGE RELAY SYSTEM.
 FT ACT_SITE 47889 48002 CHARGE RELAY SYSTEM.
 FT ACT_SITE 48003 48116 CHARGE RELAY SYSTEM.
 FT ACT_SITE 48117 48230 CHARGE RELAY SYSTEM.
 FT ACT_SITE 48231 48344 CHARGE RELAY SYSTEM.
 FT ACT_SITE 48345 48458 CHARGE RELAY SYSTEM.
 FT ACT_SITE 48459 48572 CHARGE RELAY SYSTEM.
 FT ACT_SITE 48573 48686 CHARGE RELAY SYSTEM.
 FT ACT_SITE 48687 48800 CHARGE RELAY SYSTEM.
 FT ACT_SITE 48801 48914 CHARGE RELAY SYSTEM.
 FT ACT_SITE 48915 49028 CHARGE RELAY SYSTEM.
 FT ACT_SITE 49029 49142 CHARGE RELAY SYSTEM.
 FT ACT_SITE 49143 49256 CHARGE RELAY SYSTEM.
 FT ACT_SITE 49257 49370 CHARGE RELAY SYSTEM.
 FT ACT_SITE 49371 49

RL J. Biol. Chem. 264:5957-5965(1989).
 CC -1- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
 CC (Lp(a)). It has serine proteinase activity and is able of
 CC autolysis. Inhibits tissue-type plasminogen activator 1.
 CC Lp(a) may be a ligand for megalin/Gp 330.
 CC -1- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
 CC decorin (by similarity).
 CC -1- PTM: N- and O-glycosylated (by similarity).
 CC -1- DISASE: Elevated plasma concentrations of apo(a) and its
 CC naturally occurring proteolytic fragments are correlated with
 CC atherosclerosis. Homology with plasminogen kringle IV and V is
 CC thought to underlie the atherogenicity of the protein, because the
 CC fragments are competing with plasminogen for fibrin(ogen) binding.
 CC -1- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
 CC leading to the formation of the so called mini-Lp(a). Apo(a)
 CC fragments accumulate in atherosclerotic lesions, where they may
 CC promote thrombogenesis. O-glycosylation may limit the extent of
 CC proteolytic fragmentation (by similarity).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains at least 10 kringle domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, J04635; AAA36833.1; -.
 CC PIR, A32869; A32869.
 CC HSSP, P00747; 2PK4.
 DR MEROPS, S01.226;
 DR InterPro, IPR001314; Chymotrypsin.
 DR InterPro, IPR000001; Kringle.
 DR Pfam, PF00051; kringle_11.
 DR Pfam, PF00089; trypsin_1.
 DR PRINTS, PR00722; CHYMOTRYPSIN.
 DR PRINTS, PR00018; KRINGLE.
 DR ProDom, PD000395; kringle_10.
 DR SMART, SM00130; KR, 10.
 DR SMART, SM00020; TCTP_Spc_1.
 DR PROSITE, PS00021; KRINGLE_1; 10.
 DR PROSITE, PS0070; KRINGLE_2; 10.
 DR PROSITE, PS00240; TRYPsin_DOM; 1.
 DR PROSITE, PS00134; TRYPsin_HIS; FALSE NEG.
 DR PROSITE, PS00135; TRYPsin_SER; FALSE NEG.
 KM Hydrolyase: Serine protease; Lipid transport; Plasma; Glycoprotein;
 KM Kringle; Repeat; Atherosclerosis.
 FT NON_TER 1 1
 FT DOMAIN 49 127 KRINGLE 1.
 FT DOMAIN 163 241 KRINGLE 2.
 FT DOMAIN 277 355 KRINGLE 3.
 FT DOMAIN 391 469 KRINGLE 4.
 FT DOMAIN 505 583 KRINGLE 5.
 FT DOMAIN 619 697 KRINGLE 6.
 FT DOMAIN 725 803 KRINGLE 7.
 FT DOMAIN 839 917 KRINGLE 8.
 FT DOMAIN 953 1031 KRINGLE 9.
 FT DOMAIN 1067 1145 KRINGLE 10.
 FT DOMAIN 1191 1420 KRINGLE 9.
 FT SEQUENCE 1420 AA; 158367 MW; B8102949E03C5B0E CRC64;
 SQ
 Query Match 95.5%; Score 515; DB 1; Length 1420;
 Best Local Similarity 94.5%; Pred. No. 1.7e-45;
 Matches 86; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KSPVVDCTCHGGRSRTGSSITTVTKRTQSSNIPHHHQTTPPYPAAGLTENYCNRP 60
 DB 947 KSPVVDCTCHGGRSRTGSSITTVTKRTQSSNIPHHHQTTPPYPAAGLTENYCNRP 1006
 QY 61 DSGKPCWCTTDPVCVRWEYCNLTQCSFTSG 91

DB 1007 DSGKPCWCTTDPVCVRWEYCNLTQCSFTSG 1037
 |||||
 ID PLNM MACMU .STANDARD; PRT; 810 AA.
 AC PLNM MACMU
 AD P12545;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7).
 GN PLG.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=89174660; PubMed=2925643;
 RA Tomlinson J.E., McLean J.W., Lamm R.M.;
 RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
 RT synthesis.";
 RL J. Biol. Chem. 264:5957-5965(1989).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UKRINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
 CC INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN 2 CHAINS HELD
 CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
 CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, J04697; AAA36901.1; -.
 CC PIR, B32869; B30848.
 DR HSSP, P00747; 1PMK.
 DR MEROPS, S01.233; -.
 DR InterPro, IPR001314; Chymotrypsin.
 DR InterPro, IPR000001; Kringle.
 DR InterPro, IPR003014; PAN.
 DR InterPro, IPR003609; Pan_app.
 DR InterPro, IPR003966; Prothombin.
 DR InterPro, IPR001254; Ser protease_Try.
 DR Pfam, PF00051; kringle_5.
 DR Pfam, PF00024; PAN; 1.
 DR Pfam, PF00089; trypsin_1.
 DR PRINTS, PR00722; CHYMOTRYPSIN.
 DR PRINTS, PR00018; KRINGLE.
 DR PRINTS, PR01505; PROTHROMBIN.
 DR ProDom, PD000395; Kringle_5.

| | | | |
|----|---|---------------------|---|
| DR | SMART; SMO0130; KR; 4. | PAN_AP: 1. | |
| DR | SMART; SMO0473; TYP_Spec; 1. | | |
| DR | SMART; SMO0020; TYP_Spec; 1. | | |
| DR | PROSITE; PS00021; KRINGLE_1; 5. | | |
| DR | PROSITE; PS50070; KRINGLE_2; 5. | | |
| DR | PROSITE; PS50240; TRYPSIN_DOM; 1. | | |
| DR | PROSITE; PS00134; TRYPSIN_HIS; 1. | | |
| DR | PROSITE; PS00135; TRYPSIN_SER; 1. | | |
| KM | Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis; | | |
| KM | tissue remodeling; blood coagulation; Kringle; Zymogen; Repeat; | | |
| KM | Signal. | | |
| FT | SIGNAL. | 1 | 19 |
| FT | CHAIN | 20 | 810 |
| FT | CHAIN | 20 | 580 |
| FT | PEPTIDE | 20 | 96 |
| FT | CHAIN | 97 | 580 |
| FT | CHAIN | 581 | 810 |
| FT | DOMAIN | 103 | 181 |
| FT | DOMAIN | 184 | 262 |
| FT | DOMAIN | 275 | 352 |
| FT | DOMAIN | 377 | 454 |
| FT | DOMAIN | 481 | 560 |
| FT | DOMAIN | 581 | 810 |
| FT | ACT_SITE | 622 | 622 |
| FT | ACT_SITE | 665 | 665 |
| FT | ACT_SITE | 760 | 760 |
| FT | BINDING | 136 | 136 |
| FT | BINDING | 158 | 158 |
| FT | BINDING | 172 | 172 |
| FT | BINDING | 432 | 432 |
| FT | BINDING | 445 | 445 |
| FT | BINDING | 134 | 134 |
| FT | BINDING | 136 | 136 |
| FT | DISULFID | 49 | 73 |
| FT | DISULFID | 53 | 61 |
| FT | DISULFID | 103 | 181 |
| FT | DISULFID | 124 | 164 |
| FT | DISULFID | 152 | 176 |
| FT | DISULFID | 185 | 262 |
| FT | DISULFID | 188 | 316 |
| FT | DISULFID | 206 | 245 |
| FT | DISULFID | 234 | 257 |
| FT | DISULFID | 275 | 352 |
| FT | DISULFID | 296 | 335 |
| FT | DISULFID | 324 | 347 |
| FT | DISULFID | 377 | 454 |
| FT | DISULFID | 398 | 437 |
| FT | DISULFID | 426 | 449 |
| FT | DISULFID | 481 | 560 |
| FT | DISULFID | 502 | 543 |
| FT | DISULFID | 531 | 553 |
| FT | DISULFID | 567 | 685 |
| FT | DISULFID | 577 | 585 |
| FT | DISULFID | 607 | 623 |
| FT | DISULFID | 699 | 766 |
| FT | DISULFID | 729 | 745 |
| FT | DISULFID | 756 | 784 |
| FT | CARBOHYD | 365 | 365 |
| FO | SEQUENCE | 810 AA; 90255 MM; 7 | O-LINKED (GALNAc. . .) (BY SIMILARITY). ATSELE51A1A0F24A CR664; |

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Query Match      78.8%; Score 425; DB 1; Length 810;
Best Local Similarity 77.3%; Pred. No. 1.9e-36;
Matches 68; Conservative 10; Mismatches 10; Indels 0; Gaps 0

Oy      2 SPVVDYCHGDRSRYRGISSTVTTRTCOSMSMTPHMORTPENYPNAGLTENYCRNPD 61
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      371 TPVVECHGDQDSYRGTSSITTTTGKCSOSSMTPHMHKTPEHPNNGLTMYCRNPD 430

Oy      62 SGKOPMCYTTPDCPVMEYCNIQTQCESE 89
       :|::||::||::||::||::||::||::||
Db      431 ADKGPMCFITTPDSVRMEYCNLKKCGSTE 458

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| PLAN | HUMAN | STANDARD | PRT | 810 AA. |
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| AC | P00747 | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 01-MAR-1989 (Rel. 10, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Plasminogen precursor (EC 3.4.21.7) [contains: Angiostatin]. | | | |
| GN | PLG. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=90202879; PubMed=2318846; | | | |
| RA | Petersen T.E., Matzen M.R., Ichinose A., Davie E.W.; | | | |
| RT | "Characterization of the gene for human plasminogen, a key proenzyme | | | |
| RT | in the fibrinolytic system." | | | |
| RL | J. Biol. Chem. 265:6104-6111(1990). | | | |
| RN | [2] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=87162490; PubMed=3030813; | | | |
| RA | Postgren M., Raden B., Israelsson M., Larsson K., Heden L.-O.; | | | |
| RT | "Molecular cloning and characterization of a full-length cDNA clone | | | |
| RT | for human plasminogen." | | | |
| RL | FEBS Lett. 213:254-260(1987). | | | |
| RN | [3] | | | |
| RN | SEQUENCE OF 20-810. | | | |
| RA | Sottirup-Jensen L., Petersen T.E., Magnusson S.; | | | |
| RL | Submitted (JUL-1977) to the PIR data bank. | | | |
| RN | [4] | | | |
| RN | SEQUENCE OF 292-810 FROM N.A. | | | |
| RX | MEDLINE=85023311; PubMed=6148961; | | | |
| RA | Malinowski D.P., Sadler J.E., Davie E.W.; | | | |
| RT | "Characterization of a complementary deoxyribonucleic acid coding for | | | |
| RT | human and bovine plasminogen." | | | |
| RL | Biochemistry 23:4243-4250(1984). | | | |
| RN | [5] | | | |
| RN | SEQUENCE OF 20-100. | | | |
| RX | MEDLINE=75093329; PubMed=122932; | | | |
| RA | Wiman B., Wallen P.; | | | |
| RT | "Structural relationship between 'glutamic acid' and 'lysine' forms | | | |
| RT | of human plasminogen and their interaction with the NH2-terminal | | | |
| RT | activation peptide as studied by affinity chromatography." | | | |
| RL | Eur. J. Biochem. 50:489-494(1975). | | | |
| RN | [6] | | | |
| RN | SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810. | | | |
| RA | Sottirup-Jensen L., Cleys H., Zajdel M., Petersen T.E., Magnusson S.; | | | |
| RA | (in) Davidson J.F., Rowan R.M., Samama W.M., Desnoyers P.C. (eds.); | | | |
| RL | Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209, | | | |
| RN | Raven Press, New York (1978). | | | |
| RN | [7] | | | |
| RP | SEQUENCE OF 483-604. | | | |
| RX | MEDLINE=76043692; PubMed=126863; | | | |
| RA | Wiman B., Wallen P.; | | | |
| RT | "Amino-acid sequence of the lysogen-bromide fragment from human | | | |
| RT | plasminogen that forms the linkage between the plasmin chains." | | | |
| RL | Eur. J. Biochem. 58:539-547(1975). | | | |
| RN | [8] | | | |
| RN | SEQUENCE OF 581-810. | | | |
| RX | MEDLINE=77225245; PubMed=142009; | | | |
| RA | Wiman B.; | | | |
| RT | "Primary structure of the B-chain of human plasmin." | | | |
| RL | Eur. J. Biochem. 76:129-137(1977). | | | |
| RN | [9] | | | |
| RP | ACTIVE SITE. | | | |
| RX | MEDLINE=73149248; PubMed=4694729; | | | |
| RA | Robbins K.C., Bernabe P., Arzadon L., Summaria L.; | | | |
| RT | "The primary structure of human plasminogen. II. The histidine loop | | | |
| RT | of human plasmin: light (B) chain active center histidine sequence." | | | |
| RL | J. Biol. Chem. 248:1631-1633(1973). | | | |
| RN | [10] | | | |

RP ACTIVE SITE.
RX MEDLINE=69234739; Pubmed=4240117;
RA Goshopk W.R., Summaria L., Robbins K.C.;
RT "Studies on the active center of human plasmin. Partial amino acid
sequence of a peptide containing the active center serine residue.";
RL J. Biol. Chem. 244:3590-3597(1969).
RN [11]
RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RX MEDLINE=82213905; Pubmed=6919539;
RA Trexler M., Vail Z., Patchy L.;
RT "Structure of the omega-aminocarboxylic acid-binding sites of human
plasminogen. Arginine 70 and aspartic acid 56 are essential for
binding of ligand by kringle 4.";
RL J. Biol. Chem. 257:7401-7406(1982).
RN [12]
RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RX MEDLINE=8054794; Pubmed=6094526;
RA Vail Z., Patchy L.;
RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
are essential for fibrin affinity of the kringle 1 domain.";
RL J. Biol. Chem. 259:13690-13694(1984).
RN [13]
RP PHOSPHORYLATION SITE SER-597.
RX MEDLINE=97345939; Pubmed=9201958;
RA Wang H., Proctor M., Bretthauer R.K., Castellino F.J.;
RT "Serine-578 is a major phosphorylation locus in human plasma
plasminogen.";
RL Biochemistry 36:8100-8106(1997).
RN [14]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185329; Pubmed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
plasminogen. Species specificity in relation to sialylation and
fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
RN [15]
RP CARBOHYDRATE-LINKAGE SITE SER-268.
RX MEDLINE=97207306; Pubmed=9054441;
RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Englund J.J.,
Pizzo S.V.;
RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
human plasminogen 2.";
RL J. Biol. Chem. 272:7408-7411(1997).
RN [16]
RP CHARACTERIZATION OF ANGIOSTATIN AND PARTIAL SEQUENCE.
RX MEDLINE=95042728; Pubmed=7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
suppression of metastases by a Lewis lung carcinoma.";
RL Cell 79:315-328(1994).
RN [17]
RP CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE=97238710; Pubmed=9102221;
RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
Lapevich R., Nacy C.A.;
RT "A recombinant human angiostatin protein inhibits experimental primary
and metastatic cancer.";
RL Cancer Res. 57:1329-1334(1997).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE=92031502; Pubmed=1657146;
RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
RT "Crystal and molecular structure of human plasminogen kringle 4
refined at 1.9-A resolution.";
RL Biochemistry 30:10576-10588(1991).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE=92031503; Pubmed=1657149;
RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of

RT human plasminogen kringle 4.";
RL Biochemistry 30:10589-10594(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RA Stec B., Yamano A., Whitlow M., Teeter M.M.;
RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.
A possible structural role of disordered residues.";
RL Acta Crystallogr. D 53:169-178(1997).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
RX MEDLINE=96180681; Pubmed=8611560;
RA Mathews I.I., Vanderhoff-Hanaver P., Castellino F.J., Tulinsky A.;
RT "Crystal structures of the recombinant kringle 1 domain of human
plasminogen in complexes with the ligands epsilon-aminocaproic acid
and trans-4-(aminomethyl)cyclohexane-1-carboxylic Acid.";
RL Biochemistry 35:2567-2576(1996).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
RX MEDLINE=98198034; Pubmed=9521645;
RA Chang Y., Mochalkin I., Mccance S.G., Cheng B., Tulinsky A.,
Castellino F.J.;
RT "Structure and ligand binding determinants of the recombinant kringle
5 domain of human plasminogen.";
RL Biochemistry 37:3258-3271(1998).
RN [23]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237157; Pubmed=8181475;
RA Rejante M.R., Llinas M.;
RT "1H-NMR assignments and secondary structure of human plasminogen
kringle 1.";
RL Eur. J. Biochem. 221:927-937(1994).
RN [24]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237158; Pubmed=8181476;
RA Rejante M.R., Llinas M.;
RT "Solution structure of the epsilon-aminohexanoic acid complex of
human plasminogen kringle 1.";
RL Eur. J. Biochem. 221:939-949(1994).
RN [25]
RP STRUCTURE BY NMR OF 183-354.
RX MEDLINE=96194156; Pubmed=8652577;
RA Soehndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
Rickli E.E.;
RT "Recombinant gene expression and 1H NMR characteristics of the
kringle (2 + 3) supermodule: spectroscopic/functional individuality
of plasminogen kringle domain.";
RL Biochemistry 35:2357-2364(1996).
RN [26]
RP STRUCTURE BY NMR OF 374-461.
RX MEDLINE=90219023; Pubmed=2157850;
RA Atkinson R.A., Williams R.J.P.;
RT "Solution structure of the kringle 4 domain from human plasminogen by
1H nuclear magnetic resonance spectroscopy and distance geometry.";
RL J. Mol. Biol. 212:541-552(1990).
RN [27]
RP VARIANTS PHE-374 AND THR-620.
Query Match 78.5%; Score 423; DB 1; Length 810;
Best Local Similarity 78.7%; Pred. No. 3; 1e-36;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 2 SPVDDCYHGGDSRYGISTTVTGRTGOSWSMTPHMHORTPEVYPNAGLTENYCRNPD 61
DB 371 TPVVDCTHGGDSRGTSSTTTTKKQOSWSMTPHHOKTPEVYPNAGLTENYCRNPD 430
QY 62 SCKQPCWCTTDPCEVMEYCNLTQCSSETS 90
DB 431 ADKGPWCFTTDPBSVWBYCNLKKSGTEA 459
RESULT 5
PLAN BOVIN
ID PLAN_BOVIN STANDARD; PRT; 812 AA.

AC P06868; Q28162; 06, Created)
 DT 01-JAN-1988 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 41, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7).
 GN PLG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN NCBI_TaxID=9913;
 RP TISSUE=Liver;
 RC SEQUENCE FROM N.A.
 RA Berglund L., Andersen M.D., Petersen T.E.;
 RT Cloning and characterization of the bovine plasminogen cDNA.;
 RL Int. Dairy J. 5:593-603(1995).
 RN [2]
 RN SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
 RP MEDLINE=85203906; PubMed=3846532;
 RX Schaller J., Moser P.W., Danneberg-Muller G.A.K., Rosselet S.J.,
 RA Kamper U., Rickli E.E.;
 RT "Complete amino acid sequence of bovine plasminogen. Comparison with
 human plasminogen.";
 RL Eur. J. Biochem. 149:267-278(1985).
 RN [3]
 RN SEQUENCE OF 706-812 FROM N.A.
 RP MEDLINE=85023311; PubMed=6148961;
 RX Mallinowaki D.P., Sadler J.E., Davie E.W.;
 RA "Characterization of a complementary deoxyribonucleic acid coding for
 human and bovine plasminogen.";
 RL Biochemistry 23:4243-4250(1984).
 RN [4]
 RN CARBOHYDRATE-LINKAGE SITES.
 RP MEDLINE=88185329; PubMed=3356193;
 RX Marti T., Schaller J., Rickli E.E., Schmid K., Kameiling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 plasminogen. Species specificity in relation to sialylation and
 fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 RN [5]
 RN FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION. IT WEAKENS THE WALLS OF THE
 GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 products.
 CC ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PM: N-LINKED GLYCANS CONTAIN N-ACETYLACTOSAMINE AND SIALIC ACID.
 CC O-LINKED GLYCANS CONSIST OF GAL-GALNAc DISACCHARIDE WITH IS
 CC MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
 CC MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC DR EMBL; X79402; CAAS5939.1; -;
 CC EMBL; K02935; AAA30714.1; -;

DR PIR; S45046; PLBO.
 DR HSRP; P00747; 2PK4.
 DR MEROPS; S01.233; -;
 DR GlycoSuiteDB; P06868; -;
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan. app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser. protease_Try.
 DR Pfam; PF00051; kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS50070; KRINGLE_2; 5.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Serine protease; Plasma; glycoprotein; fibrinolysis;
 KM Tissue remodeling; blood coagulation; Kringle; zymogen; Repeat;
 KM Signal.
 FT SIGNAL. 1 26
 FT CHAIN 27 812 PLASMINOGEN.
 FT CHAIN 27 583 PLASMIN HEAVY CHAIN A.
 FT CHAIN 584 812 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 110 188 KRINGLE 1.
 FT DOMAIN 192 269 KRINGLE 2.
 FT DOMAIN 282 359 KRINGLE 3.
 FT DOMAIN 384 461 KRINGLE 4.
 FT DOMAIN 485 564 KRINGLE 5.
 FT DOMAIN 584 812 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 315 315 O-LINKED (GALNAc. . .).
 FT CARBOHYD 365 365 /FTID-CAR 000015.
 FT ACT SITE 624 624 CHARGE RELAY SYSTEM.
 FT ACT SITE 667 667 CHARGE RELAY SYSTEM.
 FT ACT SITE 762 762 CHARGE RELAY SYSTEM.
 FT CONFLICT 335 335 N -> D (IN REF. 2).
 FT CONFLICT 516 516 O -> H (IN REF. 2).
 FT CONFLICT 555 555 P -> L (IN REF. 2).
 FT CONFLICT 744 744 T -> R (IN REF. 3).
 SQ SEQUENCE 812 AA; 91216 MW; 38A6A691E20946 CRC64;
 Query Match 76.6%; Score 413; DB 1; Length 812;
 Best Local Similarity 77.3%; Pred. No. 3.3e-35;
 Matches 68; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 1 KSPVDDCYHGDRSYRGISSTVTGRTGQSSWMIPIHWORTPENYPNAGLTENYCRNP 60
 DB 377 QFVPPDCYHGNGSYRGRSSSTITIRKCKQSWSMPIPHLLKTPENYPNAGLTENYCRNP 436
 QY 61 DSGKQPCWCTTTPDCVAMEYCNLTQCSST 88
 DB 437 DADKSPWCYTTPDPRVMEFCNLKCKSET 464
 RESULT 6
 PLAN_PIG STANDARD; PRT; 790 AA.
 ID PLAN_PIG
 AC P06867;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen (EC 3.4.21.7).
 GN PLG.

OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sue.
 OC NCBI_TaxID=9823;
 RN (1)
 RP SEQUENCE OF 1-560.
 RA Schaller J., Marti T., Roeselele S.J., Kaempfer U., Rickli E.E.;
 RT "Amino acid sequence of the heavy chain of porcine plasmin. Comparison
 RT of the carbohydrate attachment sites with the human and bovine
 RT species.";
 RL Fibrinolysis 1:91-102(1987).
 RN (2)
 RP SEQUENCE OF 450-790.
 RX MEDLINE=85203907; PubMed=3846533;
 RA Marti T., Schaller J., Rickli E.E.;
 RT "Determination of the complete amino-acid sequence of porcine
 RT miniplasminogen.";
 RL Eur. J. Biochem. 149:279-285(1985).
 RN (3)
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmidt K., Kamerling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to sialylation and
 RT fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAFIAAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOSINS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PTM: N-LINKED GLYCANS CONTAINS N-ACETYLACTOSAMINE, SIALIC ACID AND
 CC IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNA6
 CC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
 CC (MICROHETEROGENEITY).
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC PIR: S03733; PLRG.
 DR HSSP: P00747; SHPG.
 DR MEROPS: S01.233; -.
 DR GLYCOSULEDB: P06867; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR003966; Prochymobin.
 DR pfam: PF00024; Ser_protasee_Try.
 DR pfam: PF00024; PAN.1.
 DR pfam: PF00089; trypsin.1.
 DR PRINTS: PRO00722; CHYMOTRYPSIN.
 DR PRINTS: PRO0018; KRINGLE.
 DR PRINTS: PRO1505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle.5.
 DR SMART: SM00130; KR.5.
 DR SMART: SM00473; PAN_AP.1.
 DR SMART: SM00020; Tryp_Spc.1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS00070; KRINGLE_2; 5.
 DR PROSITE: PS02040; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.

DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Plasma: Glycoprotein; Fibrinolysis;
 KM Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
 FT CHAIN 1 560
 FT CHAIN 561 790
 FT DOMAIN 561 790
 FT DOMAIN 84 162
 FT DOMAIN 166 243
 FT DOMAIN 256 333
 FT DOMAIN 358 435
 FT DOMAIN 461 540
 FT ACT SITE 602 602
 FT ACT SITE 645 645
 FT ACT SITE 740 740
 FT CARBOHYD 289 289
 FT CARBOHYD 340 340
 FT SEQUENCE 790 AA; 88592 MW; F04EA06E74BCD58E CRC64;
 SQ
 Query Match 74.6%; Score 402; DB 1; Length 790;
 Best Local Similarity 74.2%; Pred. No. 4, 4e-34;
 Matches 66; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 QY 1 KSPVQDCYHGDRSGYRGISSTVYGRTCQSSWMIPIPHQRPENYPNAGITENYCNRP 60
 DB 351 CIPVADCCYRNGESYRGISSTVYGRTCQSSWMIPIPHQRPENYPNAGITENYCNRP 60
 QY 61 DSGKQPCWCTTDCYRWYCNLTQCSFTE 89
 DB 411 DADKSPWCYTDPRVRWEYCNLKKCSFTE 439
 RESULT 7
 PLNN MOUSE STANDARD; PRT; 812 AA.
 AC P20918; Q8C1S2; Q91WU5;
 ID 01-FEB-1991 (Rel. 17, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Plasminogen precursor (BC 3.4.21.7) [Contains: Angiostatin].
 GN PLG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91184812; PubMed=2081600;
 RA Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
 RT "Characterization of the cDNA coding for mouse plasminogen and
 RT localization of the gene to mouse chromosome 17.";
 RL Genomics 8:49-61(1990).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Brachwitz M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
 RA Nagata R.;
 RT "Genomic sequence analysis in the mouse t-complex region.";
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX PubMed=12477932;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marutina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schneetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carlini P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Guttmann J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Trichwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywincki M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences,"
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [4]
 RP SEQUENCE OF 1-16 FROM N.A.
 RC STRAIN=129/Svj; TISSUE=Liver;
 RX PubMed=12149246;
 RA Barnach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
 RA Farmer R.J., Miles L.A.,
 RA "Localisation of regulatory elements mediating constitutive and
 RT cytokine-stimulated plasminogen gene expression,"
 RL J. Biol. Chem. 277:38579-38588(2002).
 RN [5]
 RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
 RX MEDLINE=95042728; PubMed=7525077;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.,
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
 suppression of metastases by a Lewis lung carcinoma,"
 RL Cell 79:315-328(1994).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAFVIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS. SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
 CC NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
 CC METASTATIC TUMORS IN VIVO.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
 CC INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD
 CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
 CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 5 kring domains.
 CC -----
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 CC -----
 CC EMBL: J04766; AAA50168.1; -
 CC EMBL: AF481053; AAM22156.1; -
 CC EMBL: BC014773; AAH14773.1; -
 CC EMBL: AY134430; AAN15805.1; -
 CC PIR: A38514; PLMS.
 CC HSSP: P00747; 1PMK.
 CC MEROPS: S01.233; -
 CC MGD; MGI:97620; pig.
 CC GO; GO:0016506; F:apoptosis activator activity; IDA.
 CC GO; GO:0006915; P:apoptosis; IDA.
 CC InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003609; PAN.
 DR InterPro; IPR003609; PAN app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00051; kringle; 5.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00024; PAN; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KM Signal.
 FT SIGNAL. 1 19
 FT CHAIN 20 812 PLASMINOGEN.
 FT CHAIN 20 581 PLASMIN HEAVY CHAIN A.
 FT PEPTIDE 20 97 ACTIVATION PEPTIDE.
 FT CHAIN 98 581 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 98 7436 ANGIOSTATIN.
 FT CHAIN 582 812 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 103 181 KRINGLE 1.
 FT DOMAIN 184 262 KRINGLE 2.
 FT DOMAIN 275 352 KRINGLE 3.
 FT DOMAIN 377 454 KRINGLE 4.
 FT DOMAIN 481 560 KRINGLE 5.
 FT DOMAIN 582 812 SERINE PROTEASE.
 FT ACT_SITE 624 624 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 667 667 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 49 73 BY SIMILARITY.
 FT DISULFID 53 61 BY SIMILARITY.
 FT DISULFID 103 181 BY SIMILARITY.
 FT DISULFID 124 164 BY SIMILARITY.
 FT DISULFID 152 176 BY SIMILARITY.
 FT DISULFID 185 262 BY SIMILARITY.
 FT DISULFID 188 316 BY SIMILARITY.
 FT DISULFID 206 245 BY SIMILARITY.
 FT DISULFID 234 257 BY SIMILARITY.
 FT DISULFID 275 352 BY SIMILARITY.
 FT DISULFID 324 347 BY SIMILARITY.
 FT DISULFID 324 347 BY SIMILARITY.
 FT DISULFID 377 454 BY SIMILARITY.
 FT DISULFID 398 437 BY SIMILARITY.
 FT DISULFID 426 449 BY SIMILARITY.
 FT DISULFID 481 560 BY SIMILARITY.
 FT DISULFID 502 543 BY SIMILARITY.
 FT DISULFID 531 555 BY SIMILARITY.
 FT DISULFID 568 687 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 578 586 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 609 625 BY SIMILARITY.
 FT DISULFID 701 768 BY SIMILARITY.
 FT DISULFID 731 747 BY SIMILARITY.
 FT DISULFID 758 786 BY SIMILARITY.
 FT DISULFID 758 786 BY SIMILARITY.
 FT CONFLICT 235 235 R -> H (IN REF. 1).
 FT CONFLICT 525 525 G -> D (IN REF. 1).
 FT CONFLICT 649 649 S -> L (IN REF. 1).
 SQ SEQUENCE 812 AA; 90781 MW; 241732606A2FFD2 CRC64;

Query Match 72.0%; Score 388; DB 1; Length 812;
 Best Local Similarity 70.5%; Pred. No. 1,3e-32;
 Matches 62; Conservative 12; Mismatches 14; Indels 0; Gaps 0;
 QY 1 KSPVVDCHYGDGRSYRGISSTVTGRTGCSWSSMTIPHHQRTPEPNYVNAAGLTENTYCRNP 60


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Db      370 QFVVEQVQSDQSGYRGTSTTTTGKCCQSMAMFPHRSKTEBNFPAGLENNYCRNP 429
QY      61 DSGKQPMCTTDPQVMEYCNLTQCSSE 88
Db      430 DSGKQPMCTTDPQVMEYCNLTQCSSE 457

RESULT 8
PLMN_ERIEU STANDARD; PRT; 810 AA.
ID PLAN_ERIEU STANDARD; PRT; 810 AA.
AC Q29485;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7).
PLG.
OS Etrineceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96025778; PubMed=7592597;
RA Lamm R.M., Boonmark N.W., Schwartz K., Lindahl G.B., Wade D.P.,
RA Byrne C.D., Fong K.J., Meer K., Patchy L.,
RA "The recurring evolution of lipoprotein(a). Insights from cloning of
RT hedgehog apolipoprotein(a).";
RT J. Biol. Chem. 270:24004-24009(1995).
RN [2]
RP REVISIONS.
RA Lamm R.M.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION: IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kringles domains.
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CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL: U33171; AAC48717.1; -
CC PIR: I46260; I46260.
CC HSP: P00747; 1PMK.
CC MEROPS: S01.233; -
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000001; Kringles.
CC InterPro: IPR003014; PAN.
CC InterPro: IPR003609; Pan_app.
CC InterPro: IPR003966; Prothrombin.
CC InterPro: IPR001254; Ser_protease_Try.
CC Pfam: PF00051; kringles_5.
CC Pfam: PF00024; PAN; 1.

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DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR PRODOM; PD000395; Kringles; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYD_SPE; 1.
DR PROSITE; PS00020; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringles; Zymogen; Repeat;
KW Signal.
FT SIGNAL. 1 19 BY SIMILARITY.
FT CHAIN 20 810 PLASMINOGEN.
FT CHAIN 20 582 PLASMIN HEAVY CHAIN A (BY SIMILARITY).
FT CHAIN 583 810 PLASMIN LIGHT CHAIN B (BY SIMILARITY).
FT DOMAIN 583 810 SERINE PROTEASE.
FT DOMAIN 103 181 KRINGLE 1.
FT DOMAIN 185 262 KRINGLE 2.
FT DOMAIN 275 352 KRINGLE 3.
FT DOMAIN 379 456 KRINGLE 4.
FT DOMAIN 482 561 KRINGLE 5.
FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
FT CARBOHD 339 339 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 810 AA; 90902 MW; 8E75780946017A16 CRC64;

Query Match 70.1%; Score 378; DB 1; Length 810;
Best Local Similarity 68.5%; Pred. No. 1,4e-31;
Matches 61; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 KSPVQDQYHGDGSRGYSSTTVGRTQGSMSNIPMHQRTENYPAQLTENYCRNP 60
DB 372 QFVVEQVQSDQSGYRGTSTTTTGKCCQSMAMFPHRSKTEBNFPAGLENNYCRNP 431
QY 61 DSGKQPMCTTDPQVMEYCNLTQCSSE 89
DB 432 DSGKQPMCTTDPQVMEYCNLTQCSSE 460

RESULT 9
PLMN_RAT STANDARD; PRT; 169 AA.
ID PLAN_RAT STANDARD; PRT; 169 AA.
AC Q01177;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN PLG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91250378; PubMed=1645711;
RA Kanakas U.J., Makker S.P.;
RA "Identification of the rat Heymann nephritis autoantigen (GP330) as a
RT receptor site for plasminogen.";
RT J. Biol. Chem. 266:10825-10829(1991).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION: IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,

```

CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 5 kringle domains.
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, M62832; AAA1884.1; -.
 CC PIR, A40522; A40522.
 CC HSSP, P00747; 1PMK.
 CC DR MEROPS, S01.233; -.
 CC DR InterPro: IPR000001; Kringle.
 CC DR InterPro: IPR003966; Prothrombin.
 CC DR InterPro: IPR001254; Ser. protease_Try.
 CC DR Pfam, PF00051; Kringle; 2.
 CC DR PRINTS, PR00018; KRINGLE.
 CC DR PRINTS, PR01505; PROTHROMBIN.
 CC DR ProDom, PD000395; Kringle; 2.
 CC DR SMART, SM00130; KR_1.
 CC DR PROSITE, PS00021; KRINGLE_1; 1.
 CC DR PROSITE, PS50070; KRINGLE_2; 2.
 CC DR PROSITE, PS50240; TRYPSIN_DOM; PARTIAL.
 CC DR PROSITE, PS00134; TRYPSIN_HIS; PARTIAL.
 CC DR PROSITE, PS00135; TRYPSIN_SER; PARTIAL.
 CC DR HydroLase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 CC tissue remodeling; Blood coagulation; Kringle; Repeat.
 CC KM
 CC FT NON_TER 1 1
 CC FT DOMAIN <1 112 KRINGLE 3 (BY SIMILARITY).
 CC FT DOMAIN 34 112 KRINGLE 4 (BY SIMILARITY).
 CC FT DOMAIN 139 >169 KRINGLE 5 (BY SIMILARITY).
 CC FT DISULFID 34 112 BY SIMILARITY.
 CC FT DISULFID 55 95 BY SIMILARITY.
 CC FT DISULFID 83 107 BY SIMILARITY.
 CC FT NON_TER 169 169
 CC SQ SEQUENCE 169 AA; 18401 MW; 77A54214C49D010C CRC64;
 CC
 CC Query Match 67.4%; Score 363.5; DB 1; Length 169;
 CC Best Local Similarity 65.2%; Pred. No. 8.5e-31;
 CC Matches 60; Conservative 15; Mismatches 16; Indels 1; Gaps 1;
 CC
 CC Qy 1 KSPVQDCYHGDGRSYRIGISTVYTGRTCSWSSMIPHMQRPPENYPNAGLTENYCRNP 60
 CC Db 27 QTEPVQDCYHGDGRSYRIGISTVYTGRTCSWSSMIPHMQRPPENYPNAGLTENYCRNP 86
 CC Qy 61 DSGKQ-FWCYTTDPCTWMEYCNLTQCSSTSG 91
 CC Db 87 DNDQRGWCFCTTDPSTVMEYCNLTQCSSTSG 118
 CC
 CC RESULT 10
 CC HGF HUMAN STANDARD; PRT; 728 AA.
 CC ID HGF_HUMAN
 CC AC P14210; Q9BYL9; Q9UDU6;
 CC DT 01-JAN-1990 (Rel. 13, Created)
 CC DT 01-AUG-1991 (Rel. 19, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE Hepatocyte growth factor precursor (Scatter factor) (SF)
 CC DE (Hepatopoietin A).
 CC GN HGF OR HPTA.
 CC OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=91340155; PubMed=1831432; Nakamura T., Shimizu S.;
 CC RA Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;
 CC RT "Organization of the human hepatocyte growth factor-encoding gene.";
 CC RL Gene 102:213-219(1991).
 CC [2]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Placenta;
 CC RX MEDLINE=89392017; PubMed=2528952;
 CC RA Miyazawa K., Tsubouchi H., Naka D., Takahashi K., Okigaki M.,
 CC RA Arakaki N., Nakayama H., Hirose S., Sakiyama O., Takahashi K.,
 CC RA Gohda E., Daikuhara Y., Kitamura N.;
 CC RT "Molecular cloning and sequence analysis of cDNA for human hepatocyte
 CC growth factor.";
 CC RL Biochem. Biophys. Res. Commun. 163:967-973(1989).
 CC [3]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Leukocyte;
 CC RX MEDLINE=91025062; PubMed=2145836;
 CC RA Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T.,
 CC RA Asahi O., Hagiya M., Nakamura T., Shimizu S.;
 CC RT "Isolation and expression of cDNA for different forms of hepatocyte
 CC growth factor from human leukocyte.";
 CC RL Biochem. Biophys. Res. Commun. 172:321-327(1990).
 CC [4]
 CC RP SEQUENCE FROM N.A., AND SEQUENCE OF 55-73 AND 495-520.
 CC RC TISSUE=Liver;
 CC RX MEDLINE=90066676; PubMed=2531289;
 CC RA Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimonishi M.,
 CC RA Sugimura A., Tashiro K., Shimizu S.;
 CC RT "Molecular cloning and expression of human hepatocyte growth factor.";
 CC RL Nature 342:440-443(1989).
 CC [5]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Embryonic fibroblast;
 CC RX MEDLINE=9134393; PubMed=1831266;
 CC RA Weidner K.M., Arakaki N., Hartmann G., Vandekerckhove J., Weingart S.,
 CC RA Rieder H., Fomatsch C., Tsubouchi H., Hishida T., Daikuhara Y.,
 CC RA Birmeleier W.;
 CC RT "Evidence for the identity of human scatter factor and human
 CC hepatocyte growth factor.";
 CC RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005(1991).
 CC [6]
 CC RP SEQUENCE FROM N.A.
 CC RA Courtney L., Elliot G., Angell S.;
 CC RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC [7]
 CC RP SEQUENCE OF 249-695 FROM N.A.
 CC RX MEDLINE=91369928; PubMed=1832556;
 CC RA Miyazawa K., Kitamura A., Kitamura N.;
 CC RT "Structural organization and the transcription initiation site of the
 CC human hepatocyte growth factor gene.";
 CC RL Biochemistry 30:9170-9176(1991).
 CC [8]
 CC RP SIGNAL SEQUENCE CLEAVAGE SITE.
 CC RX MEDLINE=91207365; PubMed=1826837;
 CC RA Yoshizawa Y., Arakaki N., Naka D., Takahashi K., Hirose S., Kondo J.,
 CC RA Nakayama H., Gohda E., Kitamura N., Tsubouchi H., Ishii T.,
 CC RA Hishida T., Daikuhara Y.;
 CC RT "Identification of the N-terminal residue of the heavy chain of both
 CC native and recombinant human hepatocyte growth factor.";
 CC RL Biochem. Biophys. Res. Commun. 175:660-667(1991).
 CC [9]
 CC RP CARBOHYDRATE-LINKAGE SITE THR-476.
 CC RX MEDLINE=93129192; PubMed=1482348;
 CC RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
 CC RA Nakamura T., Shimizu S.;
 CC RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
 CC on the alpha chain.";

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DR EMBL; D10212; BAA01064.1; -
 DR EMBL; D10213; BAA01065.1; -
 DR EMBL; S71816; AAB31855.1; -
 DR EMBL; X72307; CAA51054.1; ALT_INIT.
 DR PIR; J02117; A60185.
 DR HSSP; P14210; IBHT.
 DR MEROPS; S01.982; -
 DR MGD; MGI:96079; Hgf.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00051; Kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS00070; KRINGLE_2; 4.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
 KW Signal; Alternative splicing; Pyroliadone carboxylic acid.
 FT SIGNAL 1 32
 FT CHAIN 33 495
 FT CHAIN 496 728
 FT MOD_RES 33 33
 FT DOMAIN 33 128
 FT DOMAIN 129 207
 FT DOMAIN 207 289
 FT DOMAIN 289 384
 FT DOMAIN 384 470
 FT DOMAIN 470 728
 FT DISULFID 71 97
 FT DISULFID 75 85
 FT DISULFID 488 607
 FT CARBOHYD 295 295
 FT CARBOHYD 403 403
 FT CARBOHYD 569 569
 FT CARBOHYD 656 656
 FT VARSPLIC 163 167
 FT CONFLICT 344 344
 FT CONFLICT 479 479
 FT CONFLICT 564 564
 FT SEQUENCE 728 AA; 82944 MW; A0381FC497534328 CRC64;
 Query Match 46.2%; Score 249; DB 1; Length 728;
 Best Local Similarity 47.6%; Pred. No. 2.6e-18;
 Matches 39; Conservative 11; Mismatches 32; Indels 0; Gaps 0;

ID HGFL_MOUSE STANDARD; PRT; 716 AA.
 AC P26928;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hepatocyte growth factor-like protein precursor (Macrophage
 DE stimulatory protein) (MSP).
 GN MST1 OR HGFL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=92002017; PubMed=1832957;
 RA Flierzer Degen S.J., Stuart L.A., Han S., Jamison C.S.;
 RT "Characterization of the mouse cDNA and gene coding for a hepatocyte
 RT growth factor-like protein: expression during development.";
 RL Biochemistry 30:9781-9791(1991).
 CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
 CC CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
 CC CONSERVED.
 CC -1- TISSUE SPECIFICITY: LIVER. LOWER LEVELS IN LUNG, PLACENTA AND
 CC ADRENAL.
 CC -1- DEVELOPMENTAL STAGE: IS EXPRESSED AT LOW LEVELS DURING GESTATION.
 CC -1- JUST BEFORE BIRTH THE LEVEL INCREASES DRAMATICALLY AND REMAINS
 CC STABLE AFTERWARDS.
 CC -1- PTM: MAY BE CLEAVED AFTER AA 488, TO YIELD A TWO-CHAIN MOLECULE
 CC HEID TOGETHER BY DISULFIDE BONDS, OR CLEAVED INTO TWO SEPARATE
 CC POLYPEPTIDES.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 4 kringle domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL; M74180; AAA50166.1; -
 DR EMBL; M74181; AAA50167.1; -
 DR HSP; P00747; IXYN.
 DR MEROPS; S01.975; -
 DR MGD; MGI:96080; Mat1.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR003966; Prothrombin.
 DR Pfam; PF00051; Kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; PROTHROMBIN.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS00070; KRINGLE_2; 4.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 KW Kringle; Glycoprotein; Serine protease homolog; Repeat; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 716
 FT DOMAIN 19 109
 FT DOMAIN 110 186
 FT DOMAIN 191 268
 FT KRINGLE 1.
 FT KRINGLE 2.

RESULT 13
 HGFL_MOUSE

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FT DOMAIN 292 370 KRINGLE 3.
FT DOMAIN 379 457 KRINGLE 4.
FT DOMAIN 489 716 SERINE PROTEASE-LIKE.
FT DISULFID 56 78 BY SIMILARITY.
FT DISULFID 60 66 BY SIMILARITY.
FT DISULFID 110 186 BY SIMILARITY.
FT DISULFID 131 169 BY SIMILARITY.
FT DISULFID 157 181 BY SIMILARITY.
FT DISULFID 191 266 BY SIMILARITY.
FT DISULFID 194 333 INTERCHAIN (BY SIMILARITY).
FT DISULFID 212 251 BY SIMILARITY.
FT DISULFID 240 263 BY SIMILARITY.
FT DISULFID 292 370 BY SIMILARITY.
FT DISULFID 313 352 BY SIMILARITY.
FT DISULFID 341 364 BY SIMILARITY.
FT DISULFID 379 457 BY SIMILARITY.
FT DISULFID 400 440 BY SIMILARITY.
FT DISULFID 428 452 BY SIMILARITY.
FT DISULFID 477 593 INTERCHAIN (BY SIMILARITY).
FT DISULFID 512 528 BY SIMILARITY.
FT DISULFID 607 672 BY SIMILARITY.
FT DISULFID 637 651 BY SIMILARITY.
FT DISULFID 662 690 BY SIMILARITY.
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 19 19 P -> Q (IN GENOMIC SEQUENCE).
SQ SEQUENCE 716 AA; 80588 MW; BHC802EP85213ACC CRC64;

Query Match 49.8%; Score 241.5; DB 1; Length 716;
Best Local Similarity 49.4%; Pred. No. 1.5e-17;
Matches 43; Conservative 9; Mismatches 34; Indels 1; Gaps 1;

Qy 4 VVQDCYHGDRSRYGISTTGTGTCQSSMSMTPHMQRTPEYVPAAGLTENYCRNPDSG 63
Db 375 VPGGCHGSGEQRGVSFKTKRGVQCCHWSSETPHKQFPPTAPQGLEANFCRNPDDG 434
Qy 64 KQ-PCWCTTDPCEWMEYCNLTQCSSE 89
Db 435 SHGPWCYTLDPDILFDYCALQRCDDQ 461

RESULT 14
PLAN_SHEEP STANDARD; PRT; 343 AA.
ID PLMN_SHEEP
AC P81286;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN Plg.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=93149995; Pubmed=1492092;
RA Schaller J., Straub C., Kamper U., Rickli B.E.;
RT "Complete amino acid sequence of ovine miniplasminogen.";
RL Protein Seq. Data Anal. 5:21-25(1992).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UNOXYGENASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble

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CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains at least 2 kringle domains.
DR PIR; B61545; B61545.
DR HSP; P00747; SHPG.
DR MEROPS; S01.233; -.
DR Interpro; IPR001314; Chymotrypsin.
DR Interpro; IPR000001; Kringle.
DR Interpro; IPR003966; Prothrombin.
DR Interpro; IPR001254; Ser protease_Try.
DR Pfam; PR00051; kringle; 1.
DR Pfam; PR00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; TRY_Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
FT NON_TER 1 1
FT DOMAIN <1 140 HEAVY CHAIN A.
FT DOMAIN 141 >343 LIGHT CHAIN A.
FT DOMAIN <1 17 KRINGLE 4.
FT DOMAIN 41 120 KRINGLE 5.
FT ACT SITE 114 341 SERINE PROTEASE.
FT ACT SITE 181 181 CHARGE RELAY SYSTEM.
FT ACT SITE 224 224 CHARGE RELAY SYSTEM.
FT ACT SITE 319 319 CHARGE RELAY SYSTEM.
FT NON_TER 343 343
SQ SEQUENCE 343 AA; 37662 MW; 8DFEB9A2D05968E0 CRC64;

Query Match 43.8%; Score 236; DB 1; Length 343;
Best Local Similarity 47.8%; Pred. No. 2.6e-17;
Matches 43; Conservative 13; Mismatches 32; Indels 2; Gaps 2;

Qy 1 KSPVVDCTHGDGRSRYGISTTGTGTCQSSMSMTPHMQRTPEYVPAAGLTENYCRN 59
Db 8 ENPEADCMIGIGCKGRKATTVAGVPCQEWAAQEPHRRGIFTPTNPAGLEKNYCRN 67
Qy 60 PDSC-KQPCWCTTDPCEWMEYCNLTQCSSE 88
Db 68 PDGDVNGPWCYTLDPDILFDYCALQRCDDQ 97

RESULT 15
PLAN_HUMAN STANDARD; PRT; 711 AA.
ID HGFL_HUMAN
AC P26927; Q13350; Q14870;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
DE stimulatory protein) (MSP) (Macrophage stimulating protein).
GN MST1 OR HGFL.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92002016; Pubmed=1655021;

```


RA Han S., Stuart L.A., Friezner Degen S.J.;
 RT "Characterization of the DNFI52 locus on human chromosome 3:
 RT identification of a gene coding for four kringle domains with
 RT homology to hepatocyte growth factor.";
 RL Biochemistry 30:9768-9780(1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93340141; PubMed=8393443;
 RA Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
 RT "Cloning, sequencing, and expression of human macrophage stimulating
 RT protein (MSP, MST1) confirms MSP as a member of the family of kringle
 RT proteins and locates the MSP gene on chromosome 3.";
 RL J. Biol. Chem. 268:15461-15468(1993).
 CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
 CC CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
 CC CONSERVED.
 CC -1- PTM: MAY BE CLEAVED AFTER AA 484, TO YIELD A TWO-CHAIN MOLECULE
 CC HELD TOGETHER BY DISULFIDE BONDS, OR TWO SEPARATE POLYPEPTIDES.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 4 kringle domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; M74178; AAA50165.1; -;
 DR EMBL; U37055; AAC50471.1; -;
 DR EMBL; L11924; AAA59872.1; -;
 DR PIR; A40331; A47136.
 DR HSSP; P00747; 2PK4.
 DR MEROPS; S01.975; -;
 DR Genew; HGNC:7380; MST1.
 DR MIM; 142408; -;
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser.protease_Try.
 DR Pfam; PF00051; kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR PRODOM; PD000395; Kringle; 4.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS00070; KRINGLE_2; 4.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR Kringle; Glycoprotein; Serine protease homolog; Repeat; Signal;
 KW Polymorphism.
 FT SIGNAL 1 18
 FT CHAIN 19 711
 FT DOMAIN 32 109
 FT DOMAIN 110 186
 FT DOMAIN 191 268
 FT DOMAIN 283 361
 FT DOMAIN 370 448
 FT DOMAIN 484 711
 FT DISULFID 56 78
 FT DISULFID 60 66
 FT DISULFID 110 186
 FT DISULFID 131 169
 FT DISULFID 157 181
 FT DISULFID 191 268
 FT POTENTIAL.
 FT HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.
 FT PAB.
 FT KRINGLE 1.
 FT KRINGLE 2.
 FT KRINGLE 3.
 FT KRINGLE 4.
 FT SERINE PROTEASE-LIKE.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.

FT DISULFID 194 324 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 212 251 BY SIMILARITY.
 FT DISULFID 240 263 BY SIMILARITY.
 FT DISULFID 283 361 BY SIMILARITY.
 FT DISULFID 304 343 BY SIMILARITY.
 FT DISULFID 332 355 BY SIMILARITY.
 FT DISULFID 370 448 BY SIMILARITY.
 FT DISULFID 391 431 BY SIMILARITY.
 FT DISULFID 419 443 BY SIMILARITY.
 FT DISULFID 468 588 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 507 523 BY SIMILARITY.
 FT DISULFID 602 667 BY SIMILARITY.
 FT DISULFID 632 646 BY SIMILARITY.
 FT DISULFID 657 685 BY SIMILARITY.
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 13 13 Y->C.
 FT VARIANT 13 13 /FTID=VAR_006631.
 FT VARIANT 212 212 C->F.
 FT VARIANT 212 212 /FTID=VAR_006632.
 FT VARIANT 676 676 E->K (IN dbSNP:7798).
 FT VARIANT 676 676 /FTID=VAR_014569.
 FT CONFLICT 623 623 L->F (IN REF. 2).
 FT SEQUENCE 711 AA; 80379 MW; 596ED21F180290E4 CRC64;
 SQ
 Query Match 42.9%; Score 231.5; DB 1; Length 711;
 Best Local Similarity 49.4%; Pred. No. 1.6e-16;
 Matches 42; Conservative 10; Mismatches 32; Indels 1; Gaps 1;
 QY 6 QDCYHGDRSYRGISSTVTGRTQSWSSMIPMHQRTPPENYPNAGLTENYCRNPDSGQ 65
 DB 368 QDCYHAGGQRYGTVSKTRKGVQCQRMASLTPHKKQFTTSEPHQLSENFGRNPDSQH 427
 QY 66 -PWCYTTDPCTAMEYCNLTQCSETE 89
 DB 428 GPWCYTMPTPTFPDYCALRRCADQ 452

Search completed: January 12, 2004, 17:23:57
 Job time : 8.86842 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:18:07 ; Search time 29.0769 Seconds
(without alignments)
807.553 Million cell updates/sec

Title: US-10-088-548-4
Perfect score: 539
Sequence: 1 KSPVVDYCHGDRSYRGIS.....DPCVRWEYCNLTQCSSESG 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 539 | 100.0 | 113 | 4 Q9UIR6 | Q9UIR6 homo sapien |
| 2 | 424 | 78.7 | 113 | 4 Q9UIR7 | Q9UIR7 homo sapien |
| 3 | 423 | 78.5 | 810 | 4 Q15146 | Q15146 homo sapien |
| 4 | 422 | 78.3 | 105 | 4 Q9UIR8 | Q9UIR8 homo sapien |
| 5 | 413 | 76.6 | 454 | 6 Q46506 | Q46506 papio hamad |
| 6 | 409 | 75.9 | 113 | 4 Q9UIR5 | Q9UIR5 homo sapien |
| 7 | 392 | 72.7 | 359 | 6 Q8WRI1 | Q8WRI1 canis fam11 |
| 8 | 391 | 72.5 | 145 | 6 Q28911 | Q28911 macaca faec |
| 9 | 388 | 72.0 | 812 | 11 Q91WJ5 | Q91WJ5 mus musculu |
| 10 | 380 | 70.5 | 132 | 4 Q16609 | Q16609 homo sapien |
| 11 | 366.5 | 68.0 | 812 | 11 Q9ROW3 | Q9ROW3 rattus norv |
| 12 | 366 | 67.9 | 806 | 6 Q18783 | Q18783 macropus eu |
| 13 | 281 | 52.1 | 2869 | 6 Q28398 | Q28398 erinaceus e |
| 14 | 272 | 50.5 | 429 | 13 Q8AVB0 | Q8AVB0 brachydanto |
| 15 | 258.5 | 48.0 | 947 | 13 Q8AXY6 | Q8AXY6 gallus galli |
| 16 | 252 | 46.8 | 285 | 4 Q8TCE2 | Q8TCE2 homo sapien |

| | | | | | |
|----|-------|------|-----|-----------|---------------------|
| 17 | 252 | 46.8 | 290 | 4 Q02935 | Q02935 homo sapien |
| 18 | 251 | 46.6 | 334 | 6 Q46507 | Q46507 papio hamad |
| 19 | 250.5 | 46.5 | 710 | 13 Q91402 | Q91402 xenopus. he |
| 20 | 250 | 46.4 | 728 | 11 Q8C9G5 | Q8C9G5 mus musculu |
| 21 | 249.5 | 46.3 | 948 | 13 Q07153 | Q07153 torpedo cal |
| 22 | 249.5 | 46.3 | 948 | 5 Q9Y1Y6 | Q9Y1Y6 ephydactia f |
| 23 | 248.5 | 46.1 | 209 | 11 Q8BS17 | Q8BS17 mus musculu |
| 24 | 248.5 | 46.1 | 313 | 13 Q9PU78 | Q9PU78 crocodylus |
| 25 | 247.5 | 45.9 | 296 | 4 Q14519 | Q14519 homo sapien |
| 26 | 246 | 45.6 | 717 | 13 P70006 | P70006 xenopus lae |
| 27 | 244 | 45.3 | 716 | 13 Q91691 | Q91691 xenopus lae |
| 28 | 243 | 45.1 | 728 | 6 Q9BH09 | Q9BH09 felis silve |
| 29 | 242.5 | 45.0 | 208 | 4 Q9BYM0 | Q9BYM0 homo sapien |
| 30 | 242.5 | 45.0 | 210 | 4 Q13494 | Q13494 homo sapien |
| 31 | 241.5 | 44.8 | 716 | 11 Q91XG8 | Q91XG8 mus musculu |
| 32 | 238.5 | 44.2 | 716 | 11 P70521 | P70521 rattus norv |
| 33 | 237.5 | 44.1 | 109 | 6 Q9W1B8 | Q9W1B8 ovis aries |
| 34 | 236.5 | 43.9 | 709 | 13 Q90ZM6 | Q90ZM6 brachydanto |
| 35 | 236 | 43.8 | 53 | 4 Q9UM12 | Q9UM12 homo sapien |
| 36 | 236 | 43.8 | 704 | 13 Q90865 | Q90865 gallus galli |
| 37 | 232.5 | 43.1 | 211 | 11 Q55027 | Q55027 mus musculu |
| 38 | 232.5 | 43.1 | 385 | 5 Q25101 | Q25101 herdmania m |
| 39 | 232 | 43.0 | 726 | 13 Q90978 | Q90978 gallus galli |
| 40 | 231.5 | 42.9 | 215 | 13 Q42341 | Q42341 gallus galli |
| 41 | 227.5 | 42.2 | 567 | 4 Q13208 | Q13208 homo sapien |
| 42 | 226.5 | 42.0 | 648 | 4 Q9H1V4 | Q9H1V4 homo sapien |
| 43 | 219 | 40.6 | 95 | 4 Q8N696 | Q8N696 homo sapien |
| 44 | 207.5 | 38.5 | 90 | 4 Q8NG20 | Q8NG20 homo sapien |
| 45 | 203.5 | 37.8 | 930 | 13 Q8AV69 | Q8AV69 xenopus lae |

ALIGNMENTS

RESULT 1
ID Q9UIR6 PRELIMINARY; PRT; 113 AA.
AC Q9UIR6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Apolipoprotein(a) (Fragment).
GN APOA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2181705; PubMed=11285247;
RA Ogoreljkova M., Kraft H.G., Ehnholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV
RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
RT different patterns in Africans and Caucasians";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL, AF158661; AAF03679.1; JOINED.
DR EMBL, AF158660; AAF03679.1; JOINED.
DR HSP, P00747; 2PK4.
DR InterPro; IPR000011; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
FT GLYCOPROTEIN; Kringle; Lipoprotein.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12697 MW; 51D4461D9C66312E CRC64;
Query Match 100.0%; Score 539; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 1e-52;

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Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSPVDDCYHGDGRSYRGISSTVTGRTCSWSSMTPHMHQRTPEYNNAGLTENYCRNP 60
DB 4 KSPVDDCYHGDGRSYRGISSTVTGRTCSWSSMTPHMHQRTPEYNNAGLTENYCRNP 63
QY 61 DSGKQPCWCTTDPQVREYCNLTQCSETESG 91
DB 64 DSGKQPCWCTTDPQVREYCNLTQCSETESG 94

RESULT 2
Q9UR7 PRELIMINARY; PRT; 113 AA.
AC Q9UR7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE Apolipoprotein(a) (Fragment).
GN APOA.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21181705; PubMed=11285247;
RA Ogorelkova M., Krat H.G., Enholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV
RT types 6 to 10 domain affect lp(a) plasma concentrations and have
RT different patterns in Africans and Caucasians.";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF158659; AAF03678.1; JOINED.
DR HSSP; P00747; 2PK4.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle.1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR GlycoProtein; Kringle; Lipoprotein.
FT NON_TER 1 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12815 MW; 4F80ADF8708548CB CRC64;

Query Match 78.7%; Score 424; DB 4; Length 113;
Best Local Similarity 78.9%; Pred. No. 7, 4e-40;
Matches 71; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 KSPVDDCYHGDGRSYRGISSTVTGRTCSWSSMTPHMHQRTPEYNNAGLTENYCRNP 60
DB 4 KSPVDDCYHGDGRSYRGISSTVTGRTCSWSSMTPHMHQRTPEYNNAGLTENYCRNP 63
QY 61 DSGKQPCWCTTDPQVREYCNLTQCSETES 90
DB 64 DSGKQPCWCTTDPQVREYCNLTQCSETES 93

RESULT 3
Q15146 PRELIMINARY; PRT; 810 AA.
AC Q15146;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Plasminogen precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Brumme M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
RA Mitchell D., Robinson J.H.;
RT "Expression of recombinant human plasminogen and aglycoplasminogen in
RT HeLa cells.";
RL Fibrinolysis 0:0-0(1991).
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL; M74220; AAA36451.1; -.
DR HSSP; P00747; 2PK4.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan. app.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser. protease_Try.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; Tryp. Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR GlycoProtein; Hydrolase; Kringle; Protease; Serine protease; Signal.
FT CHAIN 1 19 PLASMINOGEN.
FT SIGNAL 1 19
SQ SEQUENCE 810 AA; 90555 MW; B05C7DABD020B3C CRC64;

Query Match 78.5%; Score 423; DB 4; Length 810;
Best Local Similarity 78.7%; Pred. No. 8, 2e-39;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVDDCYHGDGRSYRGISSTVTGRTCSWSSMTPHMHQRTPEYNNAGLTENYCRNP 61
DB 371 TPVDDCYHGDGRSYRGISSTVTGRTCSWSSMTPHMHQRTPEYNNAGLTENYCRNP 430
QY 62 DSGKQPCWCTTDPQVREYCNLTQCSETES 90
DB 431 ADKQPCWCTTDPQVREYCNLTQCSETES 459

RESULT 4
Q9UR8 PRELIMINARY; PRT; 105 AA.
AC Q9UR8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Apolipoprotein(a) (Fragment).
GN APOA.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21181705; PubMed=11285247;
RA Ogorelkova M., Krat H.G., Enholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV
RT types 6 to 10 domain affect lp(a) plasma concentrations and have
RT different patterns in Africans and Caucasians.";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF158656; AAF03677.1; -.

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DR EMBL; AF158655; AAF03677.1; JOINED.
 DR HSSP; P00747; 2PKA.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR Glycoprotein; Kringle; Lipoprotein.
 FT NON_TER 1
 SQ SEQUENCE 105 AA; 11882 MW; 6ECB6C02CD30EFA2 CRC64;

Query Match 78.3%; Score 422; DB 4; Length 105;
 Best Local Similarity 80.0%; Pred. No. 1.2e-39;
 Matches 72; Conservative 3; Mismatches 15; Indels 0; Gaps 0;

QY 1 KSPVQDCYHGDGSRYSISSTVTGRTQSSSMIPMHQRTPEPNYAGLTENYCRNP 60
 DB 4 QSPGVQDCYHGDGSRYSISSTVTGRTQSSSMIPMHQRTPEPNYAGLTENYCRNP 63
 QY 61 DSGKQPCYTTDPCVMEYCNLTQCSETE 90
 DB 64 DAISPCYCTMDPVMWEYCNLTQCSETE 93

RESULT 5
 ID 046506 PRELIMINARY; PRT; 454 AA.
 AC 046506;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Apolipoprotein a (Fragment).
 GN BABAF0A.
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 NCBI_TaxID=9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cox L.A., Jett C., Hixson J.E.;
 RT "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
 RT Site Mutation is Associated with Deletion of a Single Exon in a Null
 RT Allele."
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 DR EMBL; AF029691; AAB97886.1; -.
 DR HSSP; P00747; 2PKA.
 DR MEROPS; S01.999; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Ser. protease_Try.
 DR Pfam; PF00051; Kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; TRY_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS00070; KRINGLE_2; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Glycoprotein; Hydroxylase; Kringle; Lipoprotein; Protease;
 KW Serine protease.
 FT NON_TER 1
 SQ SEQUENCE 454 AA; 50041 MW; 974B30744C187B2F CRC64;

Query Match 76.6%; Score 413; DB 6; Length 454;

Best Local Similarity 77.5%; Pred. No. 5.7e-38;
 Matches 69; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
 QY 1 KSPVQDCYHGDGSRYSISSTVTGRTQSSSMIPMHQRTPEPNYAGLTENYCRNP 60
 DB 95 QSPGVQDCYHGDGSRYSISSTVTGRTQSSSMIPMHQRTPEPNYAGLTENYCRNP 154
 QY 61 DSGKQPCYTTDPCVMEYCNLTQCSETE 89
 DB 155 DADTGPCFTMDPVMWEYCNLTQCSETE 183

RESULT 6
 ID 09UR5 PRELIMINARY; PRT; 113 AA.
 AC 09UR5;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (Fragment).
 GN APOA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2181705; PubMed=11285247;
 RA Ogorekova M., Kraft H.G., Ehmholm C., Utermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV
 RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
 RT different patterns in Africans and Caucasians."
 RL Hum. Mol. Genet. 10:815-824(2001).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL; AF158663; AAF03680.1; -.
 DR EMBL; AF158662; AAF03680.1; JOINED.
 DR HSSP; P00747; 1PMK.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR Glycoprotein; Kringle; Lipoprotein.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 113 AA; 12685 MW; F3D65681D9B5253A CRC64;

Query Match 75.9%; Score 409; DB 4; Length 113;
 Best Local Similarity 75.3%; Pred. No. 3.5e-38;
 Matches 67; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 KSPVQDCYHGDGSRYSISSTVTGRTQSSSMIPMHQRTPEPNYAGLTENYCRNP 60
 DB 4 QTPVVRQCYHGDGSRYSISSTVTGRTQSSSMIPMHQRTPEPNYAGLTENYCRNP 63
 QY 61 DSGKQPCYTTDPCVMEYCNLTQCSETE 89
 DB 64 DADTGPCFTMDPVMWEYCNLTQCSETE 92

RESULT 7
 ID 08WRI PRELIMINARY; PRT; 359 AA.
 AC 08WRI;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Plasminogen (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

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OX NCB1_TaxID=9615;
RN [1]
RA Fille-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O.,
RA Folkman J., Waters D.J.
RT "Angiostatin is detectable in the urine of dogs with spontaneous Bone
RT Cancer."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR EMBL; A1069985; A158519.1; -.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 4.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS50070; KRINGLE_2; 4.
KW Glycoprotein; Kringle.
FT NON_TER 1 359
SQ SEQUENCE 359 AA; 41172 MW; 776035FA80BDD9E CRC64;

Query Match 72.7%; Score 392; DB 6; Length 359;
Best Local Similarity 72.9%; Pred. No. 9,9e-36;
Matches 62; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 KSPVDDCYHGGRSRYGISTTVTGRTCSWSSMIPHHQRTPEPNAGLTENYCRNP 60
DB 275 QTPVOCYHGNGSQSYGISTTVTGRTKCSWSSMTPHREKTPENHPAGLTENYCRNP 334
QY 61 DSGKOPWCYTTPDCVREXCNLTQCS 85
DB 335 DADKSPWCYTTPDSVRWEFCNLKRC 359

RESULT 8
Q28911 PRELIMINARY; PRT; 145 AA.
ID Q28911;
AC Q28911;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Apolipoprotein[a] (Fragment).
GN APOLIPOPROTEIN[A].
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95395387; Pubmed=7666007;
RA Ramharack R., Spahr M.A., Hicks G.W., Kieft K.A., Brammer D.W.,
RA Munton L.L., Newton R.S.
RT "gemfibrozil significantly lowers cynomolgus monkey plasma
RT lipoprotein[a]-protein and liver apolipoprotein[a] mRNA levels."
RL J. Lipid Res. 36:1294-1304 (1995).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; S79621; AAD14312.1; -.
DR HSSP; P00747; 2PK4.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
KW Glycoprotein; Kringle; Lipoprotein.
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 16097 MW; 0D2DA20A06A5D87 CRC64;

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Query Match 72.5%; Score 391; DB 6; Length 145;
Best Local Similarity 75.3%; Pred. No. 4,8e-36;
Matches 67; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 KSPVDDCYHGGRSRYGISTTVTGRTCSWSSMIPHHQRTPEPNAGLTENYCRNP 60
DB 36 QSHVDDCYHGGRSQSYGISTTVTGRTQAWSSMPEPHQNTTENYCRNP 95
QY 61 DSGKOPWCYTTPDCVREXCNLTQCS 89
DB 96 DPVAPCYTTPDPNVRWEFCNLRCSDAE 124

RESULT 9
Q91WJ5 PRELIMINARY; PRT; 812 AA.
ID Q91WJ5;
AC Q91WJ5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Plasminogen.
GN Plg.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Brattwalte M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
RA Nagaraja R.;
RT "Genomic Sequence Analysis in the Mouse t-complex Region."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL; BC014773; AAH14773.1; -.
DR EMBL; AF481053; AAM22156.1; -.
DR HSSP; P00761; 1AN1.
DR MGD; MGI:97620; Plg.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003966; Prochromin.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR PRODOM; PD000395; Kringle; 5.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS50070; KRINGLE_2; 5.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolyase; Kringle; Protease; Serine protease.
SQ SEQUENCE 812 AA; 90781 MW; 24173260E6A2FED2 CRC64;

Query Match 72.0%; Score 388; DB 11; Length 812;
Best Local Similarity 70.5%; Pred. No. 6,7e-35;
Matches 62; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 1 KSPVDDCYHGGRSRYGISTTVTGRTCSWSSMIPHHQRTPEPNAGLTENYCRNP 60
DB 370 QTPVOCYHGNGSQSYGISTTVTGRTKCSWSSMTPHREKTPENHPAGLTENYCRNP 429

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QY 61 DSGKQPMCYTTDPCVMEYCNLTQCSCT 88
 DB 430 DGDGPMCYTTDPSVMEYCNLTQCSCT 457

RESULT 10
 ID 016609 PRELIMINARY; PRT; 132 AA.
 AC 016609;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 RT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DE 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 GN APOARGC.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=95268939; PubMed=7749817;
 RA Byrne C.D., Schwartz K., Lawn R.M.;
 RT "Loss of a splice donor site at a 'skipped exon' in a gene homologous
 RT to apolipoprotein(a) leads to an mRNA encoding a protein consisting of
 RT a single kringle domain."
 RL Arterioscler. Thromb. Vasc. Biol. 15:65-70(1995).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL; U19518; AAA85692.1; -;
 DR EMBL; U19517; AAA85692.1; -;
 DR HSSP; P00747; 1PMK.
 DR InterPro: IPR000001; Kringle.
 DR Pfam: PF00051; Kringle.1.
 DR PRINTS; PR00018; KRINGLE.
 DR PRODOM; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 KW Glycoprotein; Kringle.
 SQ SEQUENCE 132 AA; 1486 MW; 3794AD30A586DBA CRC64;

Query Match 70.5%; Score 380; DB 4; Length 132;
 Best Local Similarity 72.4%; Pred. No. 7.3e-35;
 Matches 63; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 3 PNVQDCYHGDGSRYSSTTGTGTCQSWSMIPMHQRTPEYCNLTQCSCT 62
 DB 23 PSVQDCYHSGOSYRGTYFTVTGRTQAWSSMTPHQSHSTPEKYENDGLISNYCNPD 82
 QY 63 GKPQPCYTTDPCVMEYCNLTQCSCT 89
 DB 83 SAGPMCYTTDPSVMEYCNLTQCSCT 109

RESULT 11
 ID 090W3 PRELIMINARY; PRT; 812 AA.
 AC 090W3;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 RT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 GN Plasminogen.
 OS Plasminogen protein precursor (EC 3.4.21.7).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Bangerter K., Johnson A.H., Thorsen S.;
 RT "Rat plasminogen: cDNA and gene structure."
 RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91250378; PubMed=1645711;
 RA Kanalas J.C., Macker S.P.;
 RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
 RT receptor site for plasminogen."
 RL J. Biol. Chem. 266:10825-10829(1991).
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 DR EMBL; AJ242649; CAB46014.1; -;
 DR HSSP; P0747; 1PMK.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan app.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR InterPro: IPR001400; Somatostatin.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR PRODOM; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN AP; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS50070; KRINGLE_2; 5.
 DR PROSITE; PS00338; SOMATOSTATIN_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein; Hydrolyase; Kringle; Protease; Serine protease; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 812 PLASMINOGEN.
 SQ SEQUENCE 812 AA; 90535 MW; 8C703C51410BCE9E CRC64;

Query Match 68.0%; Score 366.5; DB 11; Length 812;
 Best Local Similarity 66.3%; Pred. No. 1.7e-32;
 Matches 61; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

QY 1 KSPVQDCYHGDGSRYSSTTGTGTCQSWSMIPMHQRTPEYCNLTQCSCT 60
 DB 369 QTPVQDCYHSGOSYRGTYFTVTGRTQAWSSMTPHSHSTPEKYENDGLISNYCNPD 428
 QY 61 DSGKQPMCYTTDPCVMEYCNLTQCSCT 91
 DB 429 DNDGPMCYTTDPSVMEYCNLTQCSCT 460

RESULT 12
 ID 018783 PRELIMINARY; PRT; 806 AA.
 AC 018783;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 RT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DE 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 GN Plasminogen.
 OS Macropus eugenii (Tamar wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxId=9315;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98004511; PubMed=9342350;
 RA Lawn R.M., Schwartz K., Patchy L.;
 RT "Convergent evolution of apolipoprotein(a) in primates and hedgehog."
 RT Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 DR EMBL; AF012297; AAB65760.1; -;

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DR HSP; P00747; 5HPG.
DR MEROPS; S01.233; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan app.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser protease_Try.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Tryp; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYD_SPE; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR GlycoProtein; Hydrolyase; Kringle; Protease; Serine protease.
KW GlycoProtein; Hydrolyase; Kringle; Protease; Serine protease.
SQ SEQUENCE 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;

Query Match 67.9%; Score 366; DB 6; Length 806;
Best Local Similarity 63.3%; Pred. No. 1.9e-32;
Matches 57; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 KSPVQDCYHGDSRGYSSTVTYTGRTQSWSMTPHMHQRTPEYYPNAGLTENYCRNP 60
Db 364 QSVIVGECYCKGNKENTRTSTTISGKKQAWSMTHQKPPDNPVNDLRNCRNP 423
Qy 61 DSGKQPCYTTDPCVRWEYCNLTQCSSTES 90
Db 424 DGDKSPWCYTMDEPTVRWEFCNLEKSGTGS 453

RESULT 13
Q28398 PRELIMINARY; PRT; 2869 AA.
AC Q28398;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Apolipoprotein(a) (Fragment).
OS Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96025778; PubMed=7592597;
RA Lavin R.M., Boommark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
RT "The recurring evolution of lipoprotein(a). Insights from cloning of
RT hedgehog apolipoprotein(a).";
RL J. Biol. Chem. 270:24004-24009(1995).
CC -1- SIMILARITY: CONTAINS 31 KRINGLE DOMAINS.
DR EMBL; U31170; AAC48522.1; -.
DR HSP; P00747; 1PMK.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 31.
DR ProDom; PD000395; Kringle; 31.
DR SMART; SM00130; KR; 31.
DR PROSITE; PS00021; KRINGLE_1; 30.
DR PROSITE; PS00070; KRINGLE_2; 31.
KW GlycoProtein; Kringle; Lipoprotein.
FT NON TER 1
SQ SEQUENCE 2869 AA; 318601 MW; 9527CE985A4FB2A CRC64;

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Query Match 52.1%; Score 281; DB 6; Length 2869;
Best Local Similarity 51.7%; Pred. No. 2.4e-22;
Matches 45; Conservative 8; Mismatches 34; Indels 0; Gaps 0;

Qy 4 VVQDCYHGDSRGYSSTVTYTGRTQSWSMTPHMHQRTPEYYPNAGLTENYCRNPDSG 63
Db 2680 IPDQCLEGTGNGYRGSAVATVSGHTQVRWEOSPHSHRTPENYPTKLFNGYCRNPDSG 2739
Qy 64 KQPCYTTDPCVRWEYCNLTQCSSTES 90
Db 2740 VAPCCTTNSAVRWEYCKIPCSNSSS 2766

RESULT 14
Q8ABV0 PRELIMINARY; PRT; 429 AA.
ID Q8ABV0
AC Q8ABV0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Plasminogen precursor (Fragment).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanumanthiah R., Day K., Ugaadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in teleostei:
RT Evolution of coagulation factor genes and identification of zebrafish
RT factor VIIa.";
RL Blood Cells Mol. Dis. 0:0-0(2002).
DR EMBL; AF515276; AAN71006.1; -.
FT NON TER 1
SQ SEQUENCE 429 AA; 47556 MW; 9A580A214A549C12 CRC64;

Query Match 50.5%; Score 272; DB 13; Length 429;
Best Local Similarity 51.1%; Pred. No. 3.1e-22;
Matches 47; Conservative 12; Mismatches 31; Indels 2; Gaps 2;

Qy 2 SPVQDCYHGDSRGYSSTVTYTGRTQSWSMTPHMHQRTPEYYPNAGLTENYCRNP 60
Db 96 APEKCKKNGALEYRGSTMTVGTQAWSMTPHSHASFTPEYTPKGLSNCRCNP 155
Qy 61 DSG-KQPCYTTDPCVRWEYCNLTQCSSTESG 91
Db 156 DSDVNGPCYTTDPSKKMDYQQLPDCSLKCG 187

RESULT 15
Q8AXY6 PRELIMINARY; PRT; 947 AA.
ID Q8AXY6
AC Q8AXY6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Muscle-specific receptor tyrosine kinase Musk.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20538710; PubMed=11083926;
RA Ip F.C., Glase D.G., Gies D.R., Cheung J., Lai K.O., Fu A.K.,
RT "Cloning and characterization of muscle-specific kinase in chicken.";
RL Mol. Cell. Neurosci. 16:661-673(2000).
FT NON TER 12
SQ SEQUENCE FROM N.A.

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OM protein - protein search, using sw model

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(without alignments)
398.314 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1107863

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Maximum Match 100%

Listing first 45 summaries

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10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*

12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------|
| 1 | 539 | 100.0 | 91 | 22 | AAV72945 |
| 2 | 539 | 100.0 | 308 | 22 | AAV72944 |
| 3 | 425 | 78.8 | 810 | 22 | AA67228 |
| 4 | 423 | 78.5 | 280 | 20 | AAV02108 |
| 5 | 423 | 78.5 | 297 | 20 | AAV02103 |
| 6 | 423 | 78.5 | 361 | 20 | AAV08687 |
| 7 | 423 | 78.5 | 363 | 21 | AAV70255 |
| 8 | 423 | 78.5 | 364 | 20 | AAV02106 |
| 9 | 423 | 78.5 | 364 | 21 | AAV01905 |

| | | | | | | |
|----|-----|------|-----|----|----------|----------------------|
| 10 | 423 | 78.5 | 369 | 21 | AAV53868 | Amino acid sequenc |
| 11 | 423 | 78.5 | 374 | 21 | AAV79226 | Angiogenesis inhib |
| 12 | 423 | 78.5 | 375 | 21 | AAV79225 | Angiogenesis inhib |
| 13 | 423 | 78.5 | 378 | 17 | AAV07579 | Human kringlike 1-48 |
| 14 | 423 | 78.5 | 378 | 17 | AAV16450 | Human angiotensin |
| 15 | 423 | 78.5 | 378 | 23 | AAV48894 | Human angiotensin |
| 16 | 423 | 78.5 | 380 | 20 | AAV02105 | A multifunctional |
| 17 | 423 | 78.5 | 381 | 20 | AAV02101 | A multifunctional |
| 18 | 423 | 78.5 | 452 | 21 | AAV79224 | Angiogenesis inhib |
| 19 | 423 | 78.5 | 453 | 20 | AAV50501 | Amino acid sequenc |
| 20 | 423 | 78.5 | 458 | 23 | ABV75941 | Human plasminogen |
| 21 | 423 | 78.5 | 467 | 13 | AAV22499 | [GARSVQ]-(Plasmin |
| 22 | 423 | 78.5 | 476 | 13 | AAV22503 | [GARSVQ]-(Plasmin |
| 23 | 423 | 78.5 | 484 | 24 | AAV79749 | Human plasminogen |
| 24 | 423 | 78.5 | 563 | 23 | ABV75942 | Endothelial cell g |
| 25 | 423 | 78.5 | 566 | 20 | AAV02100 | A multifunctional |
| 26 | 423 | 78.5 | 571 | 23 | ABV75944 | Angiotensin-tumour |
| 27 | 423 | 78.5 | 576 | 23 | ABV75943 | Angiotensin-tumour |
| 28 | 423 | 78.5 | 790 | 15 | AAV60519 | Human 'Glu' plasmi |
| 29 | 423 | 78.5 | 790 | 22 | AAV36562 | Mammalian kringli |
| 30 | 423 | 78.5 | 791 | 18 | AAV34285 | Human plasminogen |
| 31 | 423 | 78.5 | 791 | 21 | AAV01887 | Human plasminogen |
| 32 | 423 | 78.5 | 791 | 21 | AAV9589 | Human plasminogen |
| 33 | 423 | 78.5 | 791 | 21 | AAV50867 | Human plasminogen |
| 34 | 423 | 78.5 | 791 | 22 | AAV67223 | Amino acid sequenc |
| 35 | 423 | 78.5 | 791 | 22 | AAV23660 | Human plasminogen |
| 36 | 423 | 78.5 | 791 | 24 | ABV76087 | Human plasminogen |
| 37 | 423 | 78.5 | 807 | 13 | AAV20012 | PA mutant pig 1-54 |
| 38 | 423 | 78.5 | 810 | 11 | AAV08065 | Human plasminogen |
| 39 | 423 | 78.5 | 810 | 12 | AAV13219 | R561G human plasmi |
| 40 | 423 | 78.5 | 810 | 12 | AAV12406 | R561S human plasmi |
| 41 | 423 | 78.5 | 810 | 12 | AAV13220 | Human plasminogen |
| 42 | 423 | 78.5 | 810 | 12 | AAV13221 | Human plasminogen |
| 43 | 423 | 78.5 | 810 | 12 | AAV12938 | Human plasminogen |
| 44 | 423 | 78.5 | 810 | 14 | AAV34428 | Sequence encoded p |
| 45 | 423 | 78.5 | 810 | 18 | AAV31169 | Plasminogen protei |

ALIGNMENTS

RESULT 1

AAV72945

ID AAV72945 standard; Protein; 91 AA.

XX

AC AAV72945;

XX

DT 13-JUN-2001 (first entry)

XX

DE Human apolipoprotein(a) kringlike domain IV36, LK6 protein.

XX

KW Human; angiogenesis inhibitor; LK6; apolipoprotein(a) kringlike domain;

KW angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy;

KW cystostatic; antithrombotic; antidiabetic; antiproliferative; psoriasis;

KW ocular angiogenic disease; endothelial cell proliferation; tumour;

KW cell migration.

XX

OS Homo sapiens.

XX

PN WO200119868-A1.

XX

PD 22-MAR-2001.

XX

PF 15-SEP-1999; 99WO-KR00554.

XX

PR 15-SEP-1999; 99WO-KR00554.

XX

PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.

XX

PI Chang J, Kim JS, Park EJ, Yum J, Chung S;

XX

DR WPI; 2001-244787/25.

DR N-PSDB; AAD03256.

```

XX  Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
PT  diseases, e.g. cancer and rheumatoid arthritis, has human
PT  apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
PT  sequence -
PS  Claim 1; Page 44-45; 50pp; English.
XX
CC  The present sequence is human LK6 protein which contains the amino
CC  acid sequence of human apolipoprotein(a) kringle domain IV36 (LK6
CC  (KIV36)). The human apolipoprotein(a) kringle domains IV36 (LK6
CC  protein), IV37 (LK7 protein) and V38 (LK8 protein) together form the
CC  angiogenesis inhibitor, LK68 protein. LK68, LK6, LK7 and LK8 are
CC  inhibitors are of endothelial cell proliferation, cell migration and
CC  normal development of capillaries in the chick embryo chorioallantoic
CC  membrane (CAM). LK68 protein, its single kringles or their functional
CC  equivalents, are useful for treating angiogenesis-mediated diseases,
CC  such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic
CC  disease in animals or humans. LK68 is useful as an anticancer agent and
CC  also for inhibiting primary tumour growth.
XX
SQ  Sequence 91 AA;
Query Match 100.0%; Score 539; DB 22; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSPVVDCHGGRSIRGISSTVTGRTQSWSSMIPHWQRTPEYVPAAGLTENYCRNP 60
DB 1 KSPVVDCHGGRSIRGISSTVTGRTQSWSSMIPHWQRTPEYVPAAGLTENYCRNP 60
QY 61 DSGKQPMCYTTPDCVMEYCNLTQCSERTSG 91
DB 61 DSGKQPMCYTTPDCVMEYCNLTQCSERTSG 91
RESULT 2
AA72944
ID AA72944 standard; Protein; 308 AA.
XX
AC AA72944;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human angiogenesis inhibitor, LK68 protein.
XX
KW Human; angiogenesis inhibitor; LK68; apolipoprotein(a) kringle domain;
KW angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy;
KW cytostatic; antirheumatic; antiproliferative; antiproliferative;
KW ocular angiogenic disease; endothelial cell proliferation; tumour;
KW cell migration.
XX
KM
XX
XX Homo sapiens.
XX
OS
XX
FH Key Location/Qualifiers
FT 1..91
FT /label= KIV36
FT /note= "Apolipoprotein(a) kringle domain IV36, LK6
FT protein"
FT 119..207
FT /label= KIV37
FT /note= "Apolipoprotein(a) kringle domain IV37, LK7
FT protein"
FT 223..308
FT /label= KV38
FT /note= "Apolipoprotein(a) kringle domain V38, LK8
FT protein"
XX
PN MO200119868-A1.
XX
PD 22-MAR-2001.
XX
PF 15-SEP-1999; 99WO-KR00554.

```

```

XX 15-SEP-1999; 99WO-KR00554.
XX
XX (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
PA
XX Chang J, Kim JS, Park EJ, Yum J, Chung S;
XX
XX WPI; 2001-244787/25.
DR N-PSDB; AAD03255.
XX
PT Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
PT diseases, e.g. cancer and rheumatoid arthritis, has human
PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
PT sequence -
PS Claim 4; Page 42-44; 50pp; English.
XX
XX The present sequence is human angiogenesis inhibitor, LK68 protein.
CC LK68 protein contains the amino acid sequences of human apolipoprotein(a)
CC kringle domains IV36 (LK6 protein), IV37 (LK7 protein) and V38
CC (LK8 protein). LK68, LK6, LK7 and LK8 are inhibitors are of endothelial
CC cell proliferation, cell migration and normal development of capillaries
CC in the chick embryo chorioallantoic membrane (CAM). LK68 protein, its
CC single kringles or their functional equivalents, are useful for
CC treating angiogenesis-mediated diseases, such as cancer, rheumatoid
CC arthritis, psoriasis or ocular angiogenic disease in animals or humans.
CC LK68 is useful as an anticancer agent and also for inhibiting primary
CC tumour growth.
XX
SQ Sequence 308 AA;
Query Match 100.0%; Score 539; DB 22; Length 308;
Best Local Similarity 100.0%; Pred. No. 4.8e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSPVVDCHGGRSIRGISSTVTGRTQSWSSMIPHWQRTPEYVPAAGLTENYCRNP 60
DB 1 KSPVVDCHGGRSIRGISSTVTGRTQSWSSMIPHWQRTPEYVPAAGLTENYCRNP 60
QY 61 DSGKQPMCYTTPDCVMEYCNLTQCSERTSG 91
DB 61 DSGKQPMCYTTPDCVMEYCNLTQCSERTSG 91
RESULT 3
AA67228
ID AA67228 standard; Protein; 810 AA.
XX
AC AA67228;
XX
DT 13-NOV-2001 (first entry)
XX
DE Amino acid sequence of monkey plasminogen.
XX
KW Angiotatin; plasminogen; sulfydryl donor; angiogenesis; tumour;
KW angiogenic disease; neoplastic disease; connective tissue disorder;
KW rheumatoid arthritis; atherosclerosis; ocular angiogenic disease;
KW diabetic retinopathy; corneal graft rejection; cardiovascular disease;
KW cerebral vascular disease; diabetes; immune disorder;
KW chronic inflammation; autoimmunity.
XX
KM
XX Macaca mulatta.
XX
OS
XX WO200158921-A2.
XX
PN 16-AUG-2001.
XX
PD 08-FEB-2001; 2001WO-US04021.
XX
PF 08-FEB-2000; 2000US-0500397.
XX
XX (NOUN) UNIV NORTHWESTERN.
XX
XX

```

XX WPI; 1999-255098/21.

PT New multifunctional proteins useful for treating angiogenic-mediated diseases

PS Claim 5; Page 103-104; 121pp; English.

CC The specification describes multifunctional proteins which comprise combinations of angiotatin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence represents a multifunctional protein of the invention.

SO Sequence 280 AA;

Qy Query Match 78.5%; Score 423; DB 20; Length 280;
Beat Local Similarity 78.7%; Pred. No. 2,3e-31;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0

Dy 2 SPVVOVCYHGDDRSYRGISSTVTGRTCSWSMSIPHHQRTPENYPNAGLTNYCNP 61
192 TFPVQDCYHGDGSYKSGISTTTTGKKCOSMSMTPRHOKTPEPYNAGLTMYCRNP 255

Dd 62 SGKPWCYTTPPCRWMEYNLTCSEETS 90
ADKGPWCFITTDPSVREYCNLKKGSTEA 280

RESULT 5
AA02103
ID AAY02103 standard; Protein; 297 AA.
AAY02103;
16-JUL-1999 (first entry)
A multifunctional protein of the invention.
Angiotatin; endostatin; interferon; thrombospondin;
interferon-inducible protein; platelet factor 4; anti-angiogenic;
anti-tumor; multifunctional protein; angiogenic-mediated disease;
cancer; diabetic retinopathy; macular degeneration; arthritis;
tumor cell production.
Synthetic.
OS Homo sapiens.
PN MO9916889-AI.
PD 08-APR-1999.
PF 30-SEP-1998; 98WO-US20464.
PR 01-OCT-1997; 97US-0060609.
PA (SEAR) SEARLE & CO G D.
PI Bolanowski MA, Caparon MH, Casperson GF, Gregory SA;
P1 Klein BK, McKearn JP;
DR WPI; 1999-255098/21.
XX New multifunctional proteins useful for treating angiogenic-mediated

PT diseases
 XX
 XX Claim 5; Page 99-100; 121pp; English.
 XX
 CC The specification describes multifunctional proteins which comprise
 CC combinations of angiostatin, endostatin, interferon, thrombospondin,
 CC interferon-inducible protein and platelet factor 4, and have
 CC anti-angiogenic and/or anti-tumor activity. The multifunctional protein
 CC may exhibit useful properties such as having similar or greater
 CC biological activity when compared to a single factor or by having
 CC improved half-life or decreased adverse side effects, or a combination
 CC of these properties. The proteins can be used for treating an
 CC angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular
 CC degeneration, or arthritis. They can also be used for inhibiting the
 CC production of tumor cells (characteristic of lung, breast, ovarian,
 CC prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma,
 CC hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor
 CC growth. The present sequence represents a multifunctional protein of the
 CC invention.
 CC
 SQ Sequence 297 AA;
 Query Match 78.5%; Score 423; DB 20; Length 297;
 Best Local Similarity 78.7%; Pred. No. 2,4e-31;
 Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 2 SPVVDQCYHGDGRSYRGISSTVTGRTCOSMSMIPHHORTPENYPNAGLTENYCRNP 61
 DB 209 TPVVDQCYHGDGOSYRGTSSTTTGKKCOSMSMTPRHOKTENTPNAGLTENYCRNP 268
 QY 62 SGKQPCYTTDPCVRWEYCNLTQCSETES 90
 DB 269 ADKGPWCFTTDPVSVRWEYCNLTQKCSGTEA 297
 Db
 RESULT 6
 AAY08687
 ID AAY08687 standard; Protein; 361 AA.
 XX
 AC AAY08687;
 XX
 DT 10-AUG-1999 (first entry)
 XX
 DE Human angiostatin protein fragment.
 XX
 KW Plasmidogen; human; angiostatin; endostatin; gene therapy; vector;
 KW anti-angiogenic; attenuation; cytosolic; anti-diabetic; ophthalmology;
 KW tumour growth; solid tumour; diabetic retinopathy; retina.
 XX
 OS Homo sapiens.
 XX
 PN WO9926480-A1.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-US24950.
 XX
 PR 20-NOV-1997; 97US-0975424.
 XX
 PA (GENE-) GENETIX PHARM INC.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Bachelot T, Leboulch P, Pawliuk RJ;
 XX
 DR WPI, 1999-357696/30.
 DR N-PSDB; AAX77713.
 XX
 PT Anti-angiogenic gene therapy vectors
 XX
 PS Disclosure; Page 59-60; 83pp; English.
 XX
 CC This invention describes a novel viral gene therapy vector comprising a
 CC nucleic acid molecule encoding an anti-angiogenic polypeptide chosen

CC from human or murine angiostatin, human or murine endostatin and
 CC angiogenesis-inhibiting fusions and fragments, where the viral vector is
 CC sufficiently attenuated for use in human gene therapy. The products of
 CC the invention have anti-angiogenic, cytosolic, anti-diabetic and
 CC ophthalmological activity. The vector is used in gene therapy for
 CC inhibiting tumour growth in humans harbouring a solid tumour. The vector
 CC expresses an anti-angiogenic polypeptide. An additional use comprises
 CC treatment of diabetic retinopathy, where the anti-angiogenic polypeptide
 CC inhibits angiogenesis in the vicinity of the retina. The vector is
 CC administered to cells ex vivo and then administered to the patient.
 CC
 SQ Sequence 361 AA;
 Query Match 78.5%; Score 423; DB 20; Length 361;
 Best Local Similarity 78.7%; Pred. No. 3e-31;
 Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 2 SPVVDQCYHGDGRSYRGISSTVTGRTCOSMSMIPHHORTPENYPNAGLTENYCRNP 61
 DB 273 TPVVDQCYHGDGOSYRGTSSTTTGKKCOSMSMTPRHOKTENTPNAGLTENYCRNP 332
 QY 62 SGKQPCYTTDPCVRWEYCNLTQCSETES 90
 DB 333 ADKGPWCFTTDPVSVRWEYCNLTQKCSGTEA 361
 Db
 RESULT 7
 AAY0255
 ID AAY0255 standard; Protein; 363 AA.
 XX
 AC AAY0255;
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Human angiogenesis inhibitor, angiostatin.
 XX
 KW Human; immunoglobulin gamma Fc fragment; angiostatin; immunofusion;
 KW angiogenesis; inhibitor; cytosolic; antirheumatoid; antiarthritis;
 KW antiapoptotic; antidiabetic; ophthalmological; immunosuppressant;
 KW vasotropic; vulnery; treatment; antiarteriosclerosis; tumour;
 KW metastasis; atherosclerosis; psoriasis; rheumatoid arthritis;
 KW ocular angiogenic disease; diabetic retinopathy; macular degeneration;
 KW myocardial angiogenesis; plaque neovascularization; telangiectasia;
 KW wound granulation; keloid scar; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200011033-A2.
 XX
 PD 02-MAR-2000.
 XX
 PF 25-AUG-1999; 99WO-US19329.
 XX
 PR 25-AUG-1998; 98US-0097883.
 XX
 PA (LEXI-) LEXINGEN PHARM CORP.
 XX
 PI Lo K, Li Y, Gillies SD;
 XX
 DR WPI, 2000-237616/20.
 DR N-PSDB; AAZ51295.
 XX
 PT Novel fusion protein of angiostatin or endostatin and an immunoglobulin
 PT Fc region, useful for treating conditions mediated by angiogenesis -
 PT such as rheumatoid arthritis, tumors and macular degeneration -
 XX
 PS Example 4; Pages 45-46; 68pp; English.
 XX
 CC The patent discloses a DNA molecule encoding a fusion protein comprising
 CC a signal sequence, an immunoglobulin Fc region, and an angiogenesis
 CC inhibitor selected from angiostatin, endostatin, a plasmidogen fragment
 CC having angiostatin activity, a collagen XVIII fragment having endostatin
 CC activity, or combinations of them. The fusion protein (immunofusion) is

used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis and Oeler-Weber syndrome; myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilic joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of endothelial cells, intestinal cells, atherosclerosis, sclerodermal and hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a human

angiotensin used in the construction of immunofusion containing human immunoglobulin gamma (IgG) Fc fragment.

Sequence 363 AA;

Query Match 78.5%; Score 423; DB 21; Length 363;

Best Local Similarity 78.7%; Pred. No. 3e-31; Mismatches 11; Indels 0; Gaps 0;

Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

2 SPVQDCHGDRSGYRGISSTVTGRTQSWSSMIPMHQRTPEPNYPAGLTENTYCRNP 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
275 TPVQDCHGDRSGYRGISSTVTGRTQSWSSMTPRHQKTPENYPAGLTENTYCRNP 334
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
62 SGKQPCYTTDPQVMEYCNLTQCSSETS 90
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
335 ADKGPWCFTTDPQVMEYCNLTQCSSETS 363

RESULT 8

AA02106
ID AAY02106 standard; Protein, 364 AA.

AC AAY02106;

DT 16-JUL-1999 (first entry)

DE A multifunctional protein of the invention.

Angiostatin; endostatin; interferon; thrombospondin;
interferon-inducible protein; platelet factor 4; anti-angiogenic;
anti-tumor; multifunctional protein; angiogenic-mediated disease;
cancer; diabetic retinopathy; macular degeneration; arthritis;
tumor cell production.

OS Synthetic.

OS Homo sapiens.

PN WO9916889-A1.

PD 08-APR-1999.

PF 30-SEP-1998; 98WO-US20464.

PR 01-OCT-1997; 97US-0060609.

PA (SEAR) SEARLE & CO G D.

PI Bolnowski MA, Caparon MH, Caspersen GF, Gregory SA;

PI Klein BK, McKearn UP;

DR WPI, 1999-255098/21.

PS New multifunctional proteins useful for treating angiogenic-mediated diseases

PT Claim 5; Page 101-102; 121pp; English.

XX The specification describes multifunctional proteins which comprise combinations of angiotensin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have

anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor invasion. The present sequence represents a multifunctional protein of the invention.

Sequence 364 AA;

Query Match 78.5%; Score 423; DB 20; Length 364;

Best Local Similarity 78.7%; Pred. No. 3e-31; Mismatches 11; Indels 0; Gaps 0;

Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

2 SPVQDCHGDRSGYRGISSTVTGRTQSWSSMIPMHQRTPEPNYPAGLTENTYCRNP 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
276 TPVQDCHGDRSGYRGISSTVTGRTQSWSSMTPRHQKTPENYPAGLTENTYCRNP 335
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
62 SGKQPCYTTDPQVMEYCNLTQCSSETS 90
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
336 ADKGPWCFTTDPQVMEYCNLTQCSSETS 364

RESULT 9

AAB01905
ID AAB01905 standard; Protein, 364 AA.

AC AAB01905;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringle 1-4 (angiotensin).

Plasminogen; human; kringle domain; endothelial cell proliferation;
angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
antiproliferative; antiinflammatory; antitumor; antineoplastic; antiarthritic;
antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

PR 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

PA (ABBO) ABBOTT LAB.

PI Davidson DJ;

DR WPI, 2000-349573/30.

PT Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -

PS Example 17; Page -; 48pp; English.

XX The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours

PR Use of angiotensin fragments or aggregates - for inhibiting
PT endothelial cell proliferation and treating angiotensin-mediated
PS diseases, e.g. cancer, arthritis or diabetic retinopathy

XX Claim 4; Page 140-141; 203pp; English.

CC The invention relates to new methods and compositions for
CC inhibiting endothelial cell proliferation, using as active component
CC an angiotensin fragment, a combination of angiotensin fragments, or
CC aggregate angiotensin. The fragment is preferably derived from murine,
CC human, Rhesus, porcine or bovine plasminogen and is a kringle 1,
CC kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle
CC 1-4 or kringle 1-4BKS protein. The aggregate angiotensin has a Mol. wt.
CC of 45-65 kd and is derived from a plasminogen fragment beginning at
CC approximately amino acid number 98 of murine, human, Rhesus, porcine or
CC bovine plasminogen. The active component can be used for treating
CC angiotensin-mediated diseases such as cancer, arthritis, macular
CC degeneration and diabetic retinopathy. It can also be used to develop
CC antibodies for use in diagnosis, detection and therapy.
CC The present sequence, human kringle 1-4BKS, is a specific angiotensin
CC fragment which can be used in the invention.

XX Sequence 378 AA;

Query Match 78.5%; Score 423; DB 17; Length 378;

Best Local Similarity 78.7%; Pred. No. 3.1e-31; Mismatches 11; Indels 0; Gaps 0;

Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGRSYRGISSTVTGRTCSWSSMIPMHQRTPEYVNNGLTENTYCRND 61

DB 279 TPVQDCYHGDGQSYRGISSTTTTGKCSWSSMTPRHQKTPENYNNGLTMYNCRND 338

QY 62 SGKQPCYTTDPCEVMEYCNLTQCSSETS 90

DB 339 ADKGPWCFTTDPSEVMEYCNLTQCSGTEA 367

RESULT 14

AAB16450 standard; Protein; 378 AA.

AC AAB16450;
DT 27-OCT-2000 (first entry)

XX Human angiotensin protein sequence.

XX Angiotensin-inhibiting protein receptor; angiotensin;
KW endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;
KW psoriasis; scleroderma; myocardial angiotensin; Crohn's disease;
KW cerebral collateral; arteriovenous malformation; rubeosis; cancer;
KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;
KW Helicobacter related disease; fracture; cat scratch fever.

OS Homo sapiens.

PN W0200032631-A2.

PD 08-JUN-2000.

PF 06-DEC-1999; 99MO-US28897.

PR 04-DEC-1998; 98US-0206059.

PA (ENTR-) ENTREMED INC.

PI MacDonald NJ, Sim KL;

DR WPI; 2000-412290/35.

XX New angiotensin-inhibiting protein receptors, useful in methods for
PT treating diseases and processes that are mediated by angiotensin, such
PT as solid tumours, psoriasis, scleroderma and myocardial angiotensin -

XX Disclosure, Figure 2, 100pp; English.

XX This invention relates to angiotensin-inhibiting protein receptors, and
CC the DNA sequences encoding them. Angiotensin is the generation of new
CC blood vessels into a tissue, and normally occurs in wound healing,
CC foetal and embryonal development and the formation of the corpus luteum,
CC endometrium and placenta. Angiotensin is a protein (see AAB16450 and
CC AAB68202) involved in angiotensin, and has an amino acid sequence
CC similar to that of a plasminogen fragment (see murine plasminogen
CC AAB16490). Angiotensin has the ability to inhibit angiotensin.

CC Endostatin is also an angiotensin inhibiting protein (see AAB16451 and
CC AAB68203). Sequences AAB68242 and AAB16522 represent coding and protein
CC sequences of human laminin. Laminin is an angiotensin binding protein,
CC and some of the peptides of the invention share homology with regions of
CC laminin. Peptides AAB16452-16521 (excluding AAB16490) are the
CC angiotensin-inhibiting protein receptor fragments of the invention. The
CC peptides bind either angiotensin or endostatin and can be used in methods
CC for treating diseases and processes that are mediated by angiotensin,
CC such as solid tumours, psoriasis, scleroderma, myocardial angiotensin,
CC Crohn's disease, cerebral collateral, arteriovenous malformations,
CC rubeosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,
CC Helicobacter related diseases, fractures, placental and cat scratch
CC fever. They are useful for the detection and prognosis of cancer. DNA
CC sequences A628204-A628241 encode the peptides of the invention.

XX Sequence 378 AA;

Query Match 78.5%; Score 423; DB 21; Length 378;

Best Local Similarity 78.7%; Pred. No. 3.1e-31; Mismatches 11; Indels 0; Gaps 0;

Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGRSYRGISSTVTGRTCSWSSMIPMHQRTPEYVNNGLTENTYCRND 61

DB 279 TPVQDCYHGDGQSYRGISSTTTTGKCSWSSMTPRHQKTPENYNNGLTMYNCRND 338

QY 62 SGKQPCYTTDPCEVMEYCNLTQCSSETS 90

DB 339 ADKGPWCFTTDPSEVMEYCNLTQCSGTEA 367

RESULT 15

AAM48894 standard; Protein; 378 AA.

AC AAM48894;

DT 04-APR-2002 (first entry)

XX Human angiotensin protein.

XX Human; angiotensin; endostatin; angiotensin; cancer; metastasis;
KW psoriasis; scleroderma; Crohn's disease; corneal disease;
KW retinopathy; arthritis; wound healing; Helicobacter pylori; peptic ulcer;
KW gene therapy; angiotensin antagonist; endostatin antagonist;
KW antiangiogenic; cytostatic; antiarthritis; antiinflammatory;
KW cerebroprotective; antidiabetic; vlnuicide; antipyretic; vulnerary;
KW gynaecological; cat scratch fever.

OS Homo sapiens.

PN W0200193897-A2.

PD 13-DEC-2001.

PF 04-JUN-2001; 2001MO-US17947.

PR 02-JUN-2000; 2000US-209065P.

PR 08-MAY-2001; 2001US-289387P.

PA (ENTR-) ENTREMED INC.

PI Sim KL, MacDonald NJ;

XX
DR WPI; 2002-130569/17.

XX
PT Regulating angiogenesis and treatment of angiogenesis-mediated
PT diseases, e.g. hemangioma, tumors or cancer, by administering a
PT tropomyosin binding compound or actin disrupting compound -
XX

PS Disclosure; Fig 2; 95pp; English.

XX
CC The present invention relates to methods of regulating angiogenesis in an
CC individual by administering an angiogenesis regulating composition
CC comprising a tropomyosin binding compound or an actin disrupting
CC compound. The compositions are useful for treating diseases and processes
CC mediated by angiogenesis including haemangioma, solid tumours, blood
CC borne tumours, leukaemia, metastasis, Crohn's disease, coronary or
CC cerebral collaterals, arthritis, diabetic neovascularisation, macular
CC degeneration, wound healing, Helicobacter related diseases, ovulation,
CC menstruation, and cat scratch fever. The present sequence is a protein
CC described in the exemplification of the invention.

XX
SQ Sequence 378 AA;

Query Match 78.5%; Score 423; DB 23; Length 378;
Best Local Similarity 78.7%; Pred. No. 3.1e-31;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCCYHGDGRSYRGISSTVTGRTGCSGSMI PHMHQRTPENYPNAGLTENYCRNPD 61
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
279 TPVVDCTHGDGDSYRGISSTTTGKKCSGSMTPHRHQTPEYNPNAGLTMYCRNPD 338
QY 62 SGKQPCYTTDPCVWMEYCNLTQCSSTES 90
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
339 ADKGPWCFTTDPSPVWMEYCNLTQCSSTES 367

Search completed: January 12, 2004, 17:23:21
Job time : 37.2632 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 17:24:03 ; Search time 26.6842 Seconds
(without alignments)
687.200 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539
Sequence: 1 KSPVVQDCHYHGDGRSYRGIS.....DPCVWEYCNLTQCSFTESG 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCRUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 539 | 100.0 | 1169 | 10 | US-09-870-759-126 |
| 2 | 539 | 100.0 | 1169 | 12 | US-09-751-708A-126 |
| 3 | 430 | 79.8 | 368 | 9 | US-09-761-120-42 |
| 4 | 430 | 79.8 | 368 | 12 | US-10-402-364-42 |
| 5 | 423 | 78.5 | 363 | 12 | US-10-292-418-11 |
| 6 | 423 | 78.5 | 378 | 9 | US-09-873-676-1 |
| 7 | 423 | 78.5 | 378 | 10 | US-09-335-325-42 |
| 8 | 423 | 78.5 | 391 | 15 | US-10-131-241-42 |
| 9 | 423 | 78.5 | 394 | 15 | US-10-304-287-7 |
| 10 | 423 | 78.5 | 394 | 15 | US-10-304-287-8 |
| 11 | 423 | 78.5 | 458 | 9 | US-09-946-893-4 |
| 12 | 423 | 78.5 | 569 | 9 | US-09-946-893-5 |
| 13 | 423 | 78.5 | 571 | 9 | US-09-946-893-8 |
| 14 | 423 | 78.5 | 576 | 9 | US-09-946-893-6 |
| 15 | 423 | 78.5 | 791 | 10 | US-09-967-386-1 |

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|----|-----|------|-----|----|------------------|--------------------|
| 16 | 423 | 78.5 | 791 | 15 | US-10-304-287-1 | Sequence 1, Appli |
| 17 | 423 | 78.5 | 810 | 9 | US-09-946-893-2 | Sequence 2, Appli |
| 18 | 423 | 78.5 | 810 | 12 | US-10-237-144-1 | Sequence 1, Appli |
| 19 | 423 | 78.5 | 810 | 15 | US-10-193-656-2 | Sequence 2, Appli |
| 20 | 410 | 76.1 | 352 | 9 | US-09-761-120-40 | Sequence 40, Appli |
| 21 | 410 | 76.1 | 352 | 9 | US-09-335-325-40 | Sequence 40, Appli |
| 22 | 410 | 76.1 | 352 | 12 | US-10-402-364-40 | Sequence 40, Appli |
| 23 | 410 | 76.1 | 352 | 15 | US-10-131-241-40 | Sequence 40, Appli |
| 24 | 397 | 73.7 | 364 | 15 | US-10-157-369-4 | Sequence 4, Appli |
| 25 | 397 | 73.7 | 451 | 15 | US-10-157-369-2 | Sequence 2, Appli |
| 26 | 392 | 72.7 | 359 | 12 | US-10-292-418-40 | Sequence 40, Appli |
| 27 | 388 | 72.0 | 362 | 12 | US-10-292-418-25 | Sequence 25, Appli |
| 28 | 388 | 72.0 | 378 | 9 | US-09-761-120-41 | Sequence 41, Appli |
| 29 | 388 | 72.0 | 378 | 10 | US-09-335-325-41 | Sequence 41, Appli |
| 30 | 388 | 72.0 | 378 | 12 | US-10-402-364-41 | Sequence 41, Appli |
| 31 | 388 | 72.0 | 378 | 15 | US-10-131-241-41 | Sequence 41, Appli |
| 32 | 388 | 72.0 | 459 | 9 | US-09-761-120-46 | Sequence 46, Appli |
| 33 | 388 | 72.0 | 459 | 12 | US-10-402-364-46 | Sequence 46, Appli |
| 34 | 388 | 72.0 | 812 | 9 | US-09-788-142-1 | Sequence 1, Appli |
| 35 | 388 | 72.0 | 812 | 9 | US-09-761-120-1 | Sequence 1, Appli |
| 36 | 388 | 72.0 | 812 | 9 | US-09-873-676-81 | Sequence 81, Appli |
| 37 | 388 | 72.0 | 812 | 9 | US-09-335-325-81 | Sequence 1, Appli |
| 38 | 388 | 72.0 | 812 | 12 | US-10-402-364-1 | Sequence 1, Appli |
| 39 | 388 | 72.0 | 812 | 15 | US-10-131-241-1 | Sequence 1, Appli |
| 40 | 383 | 71.1 | 78 | 9 | US-09-753-064-5 | Sequence 5, Appli |
| 41 | 383 | 71.1 | 78 | 9 | US-09-761-120-23 | Sequence 23, Appli |
| 42 | 383 | 71.1 | 78 | 10 | US-09-335-325-23 | Sequence 23, Appli |
| 43 | 383 | 71.1 | 78 | 12 | US-10-267-137-9 | Sequence 9, Appli |
| 44 | 383 | 71.1 | 78 | 12 | US-10-402-364-23 | Sequence 23, Appli |
| 45 | 383 | 71.1 | 78 | 12 | US-10-402-364-52 | Sequence 52, Appli |

ALIGNMENTS

RESULT 1
US-09-870-759-126
; Sequence 126, Application US/09870759
; Patent No. US2002017551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-126

Query Match 100.0%; Score 539; DB 10; Length 1169;
Best Local Similarity 100.0%; Pred. No. 1,1e+49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSPVVQDCHYHGDGRSYRGISSTVTGRTQSSMNIPIHQRTPEPNAGLTENYCNP 60
DB 624 KSPVVQDCHYHGDGRSYRGISSTVTGRTQSSMNIPIHQRTPEPNAGLTENYCNP 683
QY 61 DSGKOPWCYTTDPCVWEYCNLTQCSFTESG 91
DB 684 DSGKOPWCYTTDPCVWEYCNLTQCSFTESG 714

RESULT 2
US-09-751-708A-126
; Sequence 126, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:

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; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-751-708A-126

Query Match      100.0%; Score 539; DB 12; Length 1169;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSPVODCYHGDGRSYRGISSTVTGRTCSWSSMIPHHQRTPEPNYPNAGLTENYCRNP 60
Db 624 KSPVODCYHGDGRSYRGISSTVTGRTCSWSSMIPHHQRTPEPNYPNAGLTENYCRNP 603
Qy 61 DSGKQPCWCTTDPVCVRMEYCNLTQCSSETS 91
Db 684 DSGKQPCWCTTDPVCVRMEYCNLTQCSSETS 714

RESULT 3
US-09-761-120-42
; Sequence 42, Application US/09761120
; Patent No. US20020037847A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05940-0151 (43171-252068)
; CURRENT APPLICATION NUMBER: US/09/761,120
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/309,821
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 08/866,735
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Kringle 1-4 BKLS
; US-09-761-120-42

Query Match      79.8%; Score 430; DB 9; Length 368;
Best Local Similarity 79.8%; Pred. No. 2e-38;
Matches 71; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 2 SPVQDCYHGDGRSYRGISSTVTGRTCSWSSMIPHHQRTPEPNYPNAGLTENYCRNP 61
Db 269 TPVQDCYHGDGRSYRGISSTVTGRTCSWSSMTPHRQKTPENYPNAGLTENYCRNP 328
Qy 62 SGKQPCWCTTDPVCVRMEYCNLTQCSSETS 90
Db 329 ADKQPCWCTTDPVCVRMEYCNLTQCSSETS 357

RESULT 4
US-10-402-364-42
; Sequence 42, Application US/10402364
; Publication No. US20040002455A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael
; US-10-402-364-42
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; APPLICANT: Folkman, M. Judah
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05213-2151 (43170-252068)
; CURRENT APPLICATION NUMBER: US/10/402,364
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/761,120A
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/309,821
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 08/866,735
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Kringle 1-4 BKLS
; US-10-402-364-42

Query Match      79.8%; Score 430; DB 12; Length 368;
Best Local Similarity 79.8%; Pred. No. 2e-38;
Matches 71; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 2 SPVQDCYHGDGRSYRGISSTVTGRTCSWSSMIPHHQRTPEPNYPNAGLTENYCRNP 61
Db 269 TPVQDCYHGDGRSYRGISSTVTGRTCSWSSMTPHRQKTPENYPNAGLTENYCRNP 328
Qy 62 SGKQPCWCTTDPVCVRMEYCNLTQCSSETS 90
Db 329 ADKQPCWCTTDPVCVRMEYCNLTQCSSETS 357

RESULT 5
US-10-292-418-11
; Sequence 11, Application US/10292418
; Publication No. US20030139365A1
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Li, Yue
; APPLICANT: Gillies, Stephen D
; TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
; FILE REFERENCE: LEX-006C1
; CURRENT APPLICATION NUMBER: US/10/292,418
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/383,315
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US 60/097,883
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-418-11

Query Match      78.5%; Score 423; DB 12; Length 363;
Best Local Similarity 78.7%; Pred. No. 1.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 2 SPVQDCYHGDGRSYRGISSTVTGRTCSWSSMIPHHQRTPEPNYPNAGLTENYCRNP 61
Db 275 TPVQDCYHGDGRSYRGISSTVTGRTCSWSSMTPHRQKTPENYPNAGLTENYCRNP 334
Qy 62 SGKQPCWCTTDPVCVRMEYCNLTQCSSETS 90
Db 335 ADKQPCWCTTDPVCVRMEYCNLTQCSSETS 363
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: INFORMATION FOR SEQ ID NO: 42:
: SEQUENCE CHARACTERISTICS:
:     LENGTH: 378 amino acids
:     TYPE: amino acid
:     STRANDEDNESS: <Unknown>
:     TOPOLOGY: linear
:     MOLECULE TYPE: protein
:     HYPOTHEetical: NO
:     ANTI-SENSE: NO
:     FRAGMENT TYPE: N-terminal
:     ORIGINAL SOURCE:
:         ORGANISM: Homo sapiens
:     IMMEDIATE SOURCE:
:         CLONE: K1-4BXL5
: SEQUENCE DESCRIPTION: SEQ ID NO: 42:
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: US-09-335-325-42
:
Query Match          78.5%; Score 423; DB 10; Length 378;
Best Local Similarity 78.7%; Pred. No. 1,2e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVQDCYHGDGRSYRIGISSTVTGRTCSWSSMIPHHQRTPEYPNAGLTENYCRNP 61
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QY 62 SGKQPMCTTDPQVWMEYCNLTQCSSETS 90
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Db 339 ADKGPMCTTDPQVWMEYCNLTQCSGTEA 367
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RESULT 8
US-10-131-241-42
: Sequence 42, Application US/10131241
: Publication No. US20030012792A1
: GENERAL INFORMATION:
: APPLICANT: Holaday, John W.
: APPLICANT: Fortier, Anne H.
: TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
: FILE REFERENCE: 05213-0344 43170-271565
: CURRENT APPLICATION NUMBER: US/10/131,241
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: US 09/413,049
: PRIOR FILING DATE: 1999-10-06
: PRIOR APPLICATION NUMBER: US 09/316,802
: PRIOR FILING DATE: 1999-05-21
: PRIOR APPLICATION NUMBER: US 60/086,586
: PRIOR FILING DATE: 1998-05-22
: NUMBER OF SEQ ID NOS: 65
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 42
: LENGTH: 378
: TYPE: PRT
: ORGANISM: Homo sapiens
:
US-10-131-241-42

Query Match          78.5%; Score 423; DB 15; Length 378;
Best Local Similarity 78.7%; Pred. No. 1,2e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVQDCYHGDGRSYRIGISSTVTGRTCSWSSMIPHHQRTPEYPNAGLTENYCRNP 61
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Db 279 TPVVQDCYHGDGGSYRIGISSTVTGRTKCCQSWSSMTPRHQKTPENYPNAGLTWNYCRNP 338
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QY 62 SGKQPMCTTDPQVWMEYCNLTQCSSETS 90
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 339 ADKGPMCTTDPQVWMEYCNLTQCSGTEA 367
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RESULT 9
US-10-304-287-7
: Sequence 7, Application US/10304287
: Publication No. US20030083234A1

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; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; APPLICANT: Kwon, Mijung
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; FILE REFERENCE: ME02-001
; CURRENT APPLICATION NUMBER: US/10/304,287
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/333,866
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO: 7
; LENGTH: 391
; TYPE: PRT
; ORGANISM: mammalian
; US-10-304-287-7

Query Match      78.5%; Score 423; DB 15; Length 391;
Best Local Similarity 78.7%; Pred. No. 1,2e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY      2 SPVODCYHGDGSRGISTTGTGRTCCSSMIPHHORTPENYPNAGLTENYCRNDP 61
DB      275 TPVODCYHGDGSRGISTTGTGRTCCSSMTPHROKTPENYPNAGLTENYCRNDP 334
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QY      62 SGKQPCYTTDPCVRWEYCNLTQCSSETS 90
DB      335 ADKGPWCFTTDPBVRWEYCNLKKCSGTEA 363
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-10-304-287-8
; Sequence 8, Application US/10304287
; Publication No. US20030083234A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; APPLICANT: Kwon, Mijung
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; FILE REFERENCE: ME02-001
; CURRENT APPLICATION NUMBER: US/10/304,287
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/333,866
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO: 8
; LENGTH: 394
; TYPE: PRT
; ORGANISM: mammalian
; US-10-304-287-8

Query Match      78.5%; Score 423; DB 15; Length 394;
Best Local Similarity 78.7%; Pred. No. 1,3e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY      2 SPVODCYHGDGSRGISTTGTGRTCCSSMIPHHORTPENYPNAGLTENYCRNDP 61
DB      275 TPVODCYHGDGSRGISTTGTGRTCCSSMTPHROKTPENYPNAGLTENYCRNDP 334
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      62 SGKQPCYTTDPCVRWEYCNLTQCSSETS 90
DB      335 ADKGPWCFTTDPBVRWEYCNLKKCSGTEA 363
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-09-946-893-4
; Sequence 4, Application US/09946893
; Patent No. US20020072494A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Mewburn
; US-09-946-893-4
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; CURRENT APPLICATION NUMBER: US/09/946,893
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-946-893-4

Query Match      78.5%; Score 423; DB 9; Length 458;
Best Local Similarity 78.7%; Pred. No. 1,5e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY      2 SPVODCYHGDGSRGISTTGTGRTCCSSMIPHHORTPENYPNAGLTENYCRNDP 61
DB      269 TPVODCYHGDGSRGISTTGTGRTCCSSMTPHROKTPENYPNAGLTENYCRNDP 328
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      62 SGKQPCYTTDPCVRWEYCNLTQCSSETS 90
DB      329 ADKGPWCFTTDPBVRWEYCNLKKCSGTEA 357
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 12
US-09-946-893-5
; Sequence 5, Application US/09946893
; Patent No. US20020072494A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Mewburn
; CURRENT APPLICATION NUMBER: US/09/946,893
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 5
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
; US-09-946-893-5

Query Match      78.5%; Score 423; DB 9; Length 569;
Best Local Similarity 78.7%; Pred. No. 1,9e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY      2 SPVODCYHGDGSRGISTTGTGRTCCSSMIPHHORTPENYPNAGLTENYCRNDP 61
DB      371 TPVODCYHGDGSRGISTTGTGRTCCSSMTPHROKTPENYPNAGLTENYCRNDP 430
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QY      62 SGKQPCYTTDPCVRWEYCNLTQCSSETS 90
DB      431 ADKGPWCFTTDPBVRWEYCNLKKCSGTEA 459
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        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-946-893-8
; Sequence 8, Application US/09946893
; Patent No. US20020072494A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Mewburn
; CURRENT APPLICATION NUMBER: US/09/946,893
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; US-09-946-893-8
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; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
; OTHER INFORMATION: with a tumor targeting signal peptide
US-09-946-893-8

Query Match 78.5%; Score 423; DB 9; Length 571;
Best Local Similarity 78.7%; Pred. No. 1.9e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCHGDRGRYRGISSTVTGRTCOSMSMTPHMHQRTPEYPPNAGLTENTYCRNP 61
DB 371 TPVVDCHGDRGRYRGISSTVTGRTCOSMSMTPHMHQRTPEYPPNAGLTENTYCRNP 430

QY 62 SGKQPMCYTTDPCVMEYCNLTQCSSETS 90
DB 431 ADKGPWCFTTDPVSVMWEYCNLKKCSGTEA 459

RESULT 14

US-09-946-893-6
; Sequence 6, Application US/09946893
; Patent No. US2002072494A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Inhibitors
; CURRENT APPLICATION NUMBER: US/09/946,893
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
; OTHER INFORMATION: with a tumor targeting signal
US-09-946-893-6

Query Match 78.5%; Score 423; DB 9; Length 576;
Best Local Similarity 78.7%; Pred. No. 1.9e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCHGDRGRYRGISSTVTGRTCOSMSMTPHMHQRTPEYPPNAGLTENTYCRNP 61
DB 371 TPVVDCHGDRGRYRGISSTVTGRTCOSMSMTPHMHQRTPEYPPNAGLTENTYCRNP 430

QY 62 SGKQPMCYTTDPCVMEYCNLTQCSSETS 90
DB 431 ADKGPWCFTTDPVSVMWEYCNLKKCSGTEA 459

RESULT 15

US-09-967-386-1
; Sequence 1, Application US/09967386
; Patent No. US2002015992A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Henkin, Jack
; APPLICANT: Davidson, Donald J.
; TITLE OF INVENTION: ANTIANGIOGENIC POLYPEPTIDES AND METHODS
; TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
; FILE REFERENCE: 6738 US.02

; CURRENT APPLICATION NUMBER: US/09/967,386
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/236,550
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-967-386-1

Query Match 78.5%; Score 423; DB 10; Length 791;
Best Local Similarity 78.7%; Pred. No. 2.6e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCHGDRGRYRGISSTVTGRTCOSMSMTPHMHQRTPEYPPNAGLTENTYCRNP 61
DB 352 TPVVDCHGDRGRYRGISSTVTGRTCOSMSMTPHMHQRTPEYPPNAGLTENTYCRNP 411

QY 62 SGKQPMCYTTDPCVMEYCNLTQCSSETS 90
DB 412 ADKGPWCFTTDPVSVMWEYCNLKKCSGTEA 440

Search completed: January 12, 2004, 17:29:39
Job time : 27.6842 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 17:21:34 : Search time 13 Seconds
(without alignments)
296.176 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539
Sequence: 1 KSPVQDCHGDGRSYRGIS.....DPCVMEYCNLTQCESTESG 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgnt2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgnt2_6/prodata/1/1aa/5B_COMB.pep:*
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- 4: /cgnt2_6/prodata/1/1aa/5B_COMB.pep:*
- 5: /cgnt2_6/prodata/1/1aa/5A_COMB.pep:*
- 6: /cgnt2_6/prodata/1/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|-------|-------------------------------------|
| 1 | 425 | 78.8 | 810 4 | US-08-991-761A-11 Sequence 11, Appl |
| 2 | 423 | 78.5 | 374 4 | US-09-377-250-3 Sequence 3, Appl |
| 3 | 423 | 78.5 | 375 4 | US-09-377-250-2 Sequence 2, Appl |
| 4 | 423 | 78.5 | 378 2 | US-08-612-788-42 Sequence 42, Appl |
| 5 | 423 | 78.5 | 378 3 | US-09-066-028-42 Sequence 42, Appl |
| 6 | 423 | 78.5 | 378 3 | US-09-066-059-1 Sequence 1, Appl |
| 7 | 423 | 78.5 | 378 4 | US-09-335-325-42 Sequence 42, Appl |
| 8 | 423 | 78.5 | 451 4 | US-09-377-250-1 Sequence 1, Appl |
| 9 | 423 | 78.5 | 452 4 | US-09-377-250-1 Sequence 4, Appl |
| 10 | 423 | 78.5 | 790 2 | US-08-469-486-54 Sequence 54, Appl |
| 11 | 423 | 78.5 | 790 2 | US-08-469-658-54 Sequence 54, Appl |
| 12 | 423 | 78.5 | 791 1 | US-08-643-219-1 Sequence 1, Appl |
| 13 | 423 | 78.5 | 791 2 | US-09-131-995-1 Sequence 1, Appl |
| 14 | 423 | 78.5 | 791 3 | US-08-832-087B-1 Sequence 1, Appl |
| 15 | 423 | 78.5 | 791 3 | US-08-851-350-1 Sequence 1, Appl |
| 16 | 423 | 78.5 | 791 3 | US-09-132-154-1 Sequence 1, Appl |
| 17 | 423 | 78.5 | 791 4 | US-08-991-761A-6 Sequence 6, Appl |
| 18 | 423 | 78.5 | 810 1 | US-07-854-603-2 Sequence 2, Appl |
| 19 | 423 | 78.5 | 810 3 | US-08-147-000B-29 Sequence 29, Appl |
| 20 | 423 | 78.5 | 810 3 | US-09-086-514-1 Sequence 1, Appl |
| 21 | 423 | 78.5 | 810 4 | US-09-192-012-5 Sequence 5, Appl |
| 22 | 423 | 78.5 | 810 6 | US-09-335-325-40 Sequence 40, Appl |
| 23 | 423 | 78.5 | 814 1 | US-08-750-711-1 Sequence 1, Appl |
| 24 | 413 | 76.6 | 812 4 | US-08-991-761A-7 Sequence 7, Appl |
| 25 | 410 | 76.1 | 352 2 | US-08-612-788-40 Sequence 40, Appl |
| 26 | 410 | 76.1 | 352 3 | US-09-066-028-40 Sequence 40, Appl |
| 27 | 410 | 76.1 | 352 4 | US-09-335-325-40 Sequence 40, Appl |

| | | | | |
|----|-----|------|-------|-------------------------------------|
| 28 | 405 | 75.1 | 84 4 | US-09-348-953-2 Sequence 2, Appl |
| 29 | 402 | 74.6 | 790 4 | US-08-991-761A-13 Sequence 13, Appl |
| 30 | 388 | 72.0 | 378 4 | US-08-612-788-41 Sequence 41, Appl |
| 31 | 388 | 72.0 | 378 3 | US-09-066-028-41 Sequence 41, Appl |
| 32 | 388 | 72.0 | 378 4 | US-09-335-325-41 Sequence 41, Appl |
| 33 | 388 | 72.0 | 398 4 | US-09-192-012-2 Sequence 1, Appl |
| 34 | 388 | 72.0 | 812 1 | US-08-451-932-1 Sequence 1, Appl |
| 35 | 388 | 72.0 | 812 1 | US-08-451-932-1 Sequence 1, Appl |
| 36 | 388 | 72.0 | 812 1 | US-08-451-932-1 Sequence 1, Appl |
| 37 | 388 | 72.0 | 812 1 | US-08-326-785-1 Sequence 1, Appl |
| 38 | 388 | 72.0 | 812 2 | US-08-612-788-1 Sequence 1, Appl |
| 39 | 388 | 72.0 | 812 2 | US-08-605-598B-1 Sequence 1, Appl |
| 40 | 388 | 72.0 | 812 2 | US-08-429-743-1 Sequence 1, Appl |
| 41 | 388 | 72.0 | 812 2 | US-08-866-735-1 Sequence 1, Appl |
| 42 | 388 | 72.0 | 812 3 | US-09-066-028-1 Sequence 1, Appl |
| 43 | 388 | 72.0 | 812 4 | US-09-192-012-3 Sequence 3, Appl |
| 44 | 388 | 72.0 | 812 4 | US-09-335-325-1 Sequence 1, Appl |
| 45 | 388 | 72.0 | 812 4 | US-08-991-761A-12 Sequence 12, Appl |

ALIGNMENTS

RESULT 1
US-08-991-761A-11
Sequence 11, Application US/08991761A
Patent No. 6576609
GENERAL INFORMATION:
APPLICANT: Soft, Gerald
APPLICANT: Gately, Stephen
TITLE OF INVENTION: "Methods and Compositions for Generating
TITLE OF INVENTION: Angiotensin"
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rose P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,761A
FILING DATE:
CLASSIFICATION: 1642
ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wanneil M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3501-16-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 810 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-991-761A-11
Query Match 78.8%: Score 425; DB 4; Length 810;
Beet Local Similarity 77.3%: Pred. No. 1.3e-37;
Matches 68; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
QY 2 SPVVDCHGDGRSYRGISITVTGRTCSWSSMIPHWQRTPEVNYAGLTENTYCRND 61
DB 371 TPVVDCHGDGRSYRGISITVTGRTCSWSSMIPHWQRTPEVNYAGLTENTYCRND 430

QY 62 SGKQPCWCTTDPQVRWEYCNLTQCSGTE 89
DB 431 ADKGPWCFTTDPQVRWEYCNLTQCSGTE 458

RESULT 2

US-09-377-250-3
Sequence 3, Application US/09377250
Patent No. 6365364
GENERAL INFORMATION:
APPLICANT: MANN, KENNETH G.
APPLICANT: SMORDS JENNY, NANCY
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
FILE REFERENCE: 48409/360
CURRENT APPLICATION NUMBER: US/09/377,250
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 374
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: angiogenesis inhibitor
NAME/KEY: MOD RES
LOCATION: (264)
OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-3

Query Match 78.5%; Score 423; DB 4; Length 374;
Best Local Similarity 78.7%; Pred. No. 8.8e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 61
DB 274 TPVQDCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 333

QY 62 SGKQPCWCTTDPQVRWEYCNLTQCSGTE 90
DB 334 ADKGPWCFTTDPQVRWEYCNLTQCSGTE 362

RESULT 3

US-09-377-250-2
Sequence 2, Application US/09377250
Patent No. 6365364
GENERAL INFORMATION:
APPLICANT: MANN, KENNETH G.
APPLICANT: SMORDS JENNY, NANCY
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
FILE REFERENCE: 48409/360
CURRENT APPLICATION NUMBER: US/09/377,250
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: angiogenesis inhibitor
NAME/KEY: MOD RES
LOCATION: (265)
OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-2

Query Match 78.5%; Score 423; DB 4; Length 375;
Best Local Similarity 78.7%; Pred. No. 8.8e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 61
DB 275 TPVQDCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 334

QY 62 SGKQPCWCTTDPQVRWEYCNLTQCSGTE 90
DB 335 ADKGPWCFTTDPQVRWEYCNLTQCSGTE 363

RESULT 4

US-08-612-788-42
Sequence 42, Application US/08612788
Patent No. 5837682
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: KL-4BKLS
US-08-612-788-42

Query Match 78.5%; Score 423; DB 2; Length 378;
Best Local Similarity 78.7%; Pred. No. 8.9e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 61
DB 279 TPVQDCYHGDGRSYRGISSTVTGRTQCSWSSMTPHHQRTPEYNNAGLTENYCRND 338

QY 62 SGKQPCWCTTDPQVRWEYCNLTQCSGTE 90
DB 339 ADKGPWCFTTDPQVRWEYCNLTQCSGTE 367

RESULT 5

US-09-066-028-42
; Sequence 42, Application US/09066028
; Patent No. 6024688
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, B. Kim Lee
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/066,028
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714
; REFERENCE/DOCKET NUMBER: 05213-0126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: K1-4BKLS
; US-09-066-028-42

Query Match 78.5%; Score 423; DB 3; Length 378;
Best Local Similarity 78.7%; Pred. No. 8.9e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVQDCYHGDGSGYRGISSTTTGRTGQSSMTPHMHQRTPEYPPNAGLTENYCRNPD 61
DB 279 TPVVQDCYHGDGSGYRGISSTTTGRTGQSSMTPHMHQRTPEYPPNAGLTENYCRNPD 338

QY 62 SGKOPWCYTTDPCVWWEYCNLTQCSSETS 90
DB 339 ADKGPWCFTTDPVSWEYCNLTQCSSETS 367

RESULT 6
US-09-206-059-1
; Sequence 1, Application US/09206059
; Patent No. 6201104
; GENERAL INFORMATION:
; APPLICANT: Macdonald, Nicholas
; APPLICANT: Sim, Kim Lee
; TITLE OF INVENTION: Angiogenesis-inhibiting Protein Binding Peptides and

; TITLE OF INVENTION: Proteins and Methods of Use
; FILE REFERENCE: 05213-0370
; CURRENT APPLICATION NUMBER: US/09/206,059
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-206-059-1

Query Match 78.5%; Score 423; DB 3; Length 378;
Best Local Similarity 78.7%; Pred. No. 8.9e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVQDCYHGDGSGYRGISSTTTGRTGQSSMTPHMHQRTPEYPPNAGLTENYCRNPD 61
DB 279 TPVVQDCYHGDGSGYRGISSTTTGRTGQSSMTPHMHQRTPEYPPNAGLTENYCRNPD 338

QY 62 SGKOPWCYTTDPCVWWEYCNLTQCSSETS 90
DB 339 ADKGPWCFTTDPVSWEYCNLTQCSSETS 367

RESULT 7
US-09-335-325-42
; Sequence 42, Application US/09335325
; Patent No. 6521439
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, B. Kim Lee
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/335,325
; FILING DATE: 17-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,788
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714
; REFERENCE/DOCKET NUMBER: 05213-0126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K1-48LJS
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-335-325-42

Query Match 78.5%; Score 423; DB 4; Length 378;
Best Local Similarity 78.7%; Pred. No. 8.9e-38;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCCYHGDGSRYSIGSTTGTGTCOSWSSMTPHMQRTPEPNAGLTENYCRNP 61
DB 279 TPVVDCCYHGDGSRYSIGSTTGTGTCOSWSSMTPHMQRTPEPNAGLTENYCRNP 338

QY 62 SGKOPWCYTTDPCVRMEYCNLTQCSSETS 90
DB 339 ADKGPWCFTTDPVSVMYCNLKKCSGTEA 367

RESULT 8

US-09-377-250-1
Sequence 1, Application US/09377250
Patent No. 6365364
GENERAL INFORMATION:
APPLICANT: MANN, KENNETH G.
APPLICANT: SMORDS JENNY, NANCY
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
FILE REFERENCE: 48409/360
CURRENT APPLICATION NUMBER: US/09/377,250
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: plasminogen fragment
FEATURE:
NAME/KEY: MOD RES
LOCATION: (53)
OTHER INFORMATION: Xaa = Gln or Glu
NAME/KEY: MOD RES
LOCATION: (341)
OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-1

Query Match 78.5%; Score 423; DB 4; Length 451;
Best Local Similarity 78.7%; Pred. No. 1.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCCYHGDGSRYSIGSTTGTGTCOSWSSMTPHMQRTPEPNAGLTENYCRNP 61
DB 351 TPVVDCCYHGDGSRYSIGSTTGTGTCOSWSSMTPHMQRTPEPNAGLTENYCRNP 410

QY 62 SGKOPWCYTTDPCVRMEYCNLTQCSSETS 90
DB 411 ADKGPWCFTTDPVSVMYCNLKKCSGTEA 439

RESULT 9

US-09-377-250-4
Sequence 4, Application US/09377250
Patent No. 6365364
GENERAL INFORMATION:
APPLICANT: MANN, KENNETH G.
APPLICANT: SMORDS JENNY, NANCY
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
FILE REFERENCE: 48409/360
CURRENT APPLICATION NUMBER: US/09/377,250
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 4
LENGTH: 452
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: plasminogen fragment
FEATURE:
NAME/KEY: MOD RES
LOCATION: (53)
OTHER INFORMATION: Xaa = Gln or Glu
NAME/KEY: MOD RES
LOCATION: (342)
OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-4

Query Match 78.5%; Score 423; DB 4; Length 452;
Best Local Similarity 78.7%; Pred. No. 1.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVVDCCYHGDGSRYSIGSTTGTGTCOSWSSMTPHMQRTPEPNAGLTENYCRNP 61
DB 352 TPVVDCCYHGDGSRYSIGSTTGTGTCOSWSSMTPHMQRTPEPNAGLTENYCRNP 411

QY 62 SGKOPWCYTTDPCVRMEYCNLTQCSSETS 90
DB 412 ADKGPWCFTTDPVSVMYCNLKKCSGTEA 440

RESULT 10

US-08-469-486-54
Sequence 54, Application US/08469486
Patent No. 5739281
GENERAL INFORMATION:
APPLICANT: Thoegeisen, Hans Christian
APPLICANT: Hollet, Thor Laas
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-486-54

Query Match 78.5%; Score 423; DB 1; Length 790;
Best Local Similarity 78.7%; Pred. No. 2.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHQKTPENYPNAGLTMYNCRND 61
DB 351 TPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHQKTPENYPNAGLTMYNCRND 410
QY 62 SGKQPMCYTTDPCVMEYCNLTQCSSETS 90
DB 411 ADKGPWCFTTDBSVMEYCNLKKCSGTEA 439

RESULT 11
US-08-469-658-54
Sequence 54, Application US/08469658
Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: Th egersten, Hans Christian
APPLICANT: Holter, Thor Las
APPLICANT: Ezerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-658-54

Query Match 78.5%; Score 423; DB 2; Length 790;
Best Local Similarity 78.7%; Pred. No. 2.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 2 SPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHQKTPENYPNAGLTMYNCRND 61
DB 351 TPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHQKTPENYPNAGLTMYNCRND 410

DB 351 TPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHQKTPENYPNAGLTMYNCRND 410
QY 62 SGKQPMCYTTDPCVMEYCNLTQCSSETS 90
DB 411 ADKGPWCFTTDBSVMEYCNLKKCSGTEA 439

RESULT 12
US-08-643-219-1
Sequence 1, Application US/08643219
Patent No. 5801146
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,219
FILING DATE: 06-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Casulo, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 791 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
US-08-643-219-1

Query Match 78.5%; Score 423; DB 1; Length 791;
Best Local Similarity 78.7%; Pred. No. 2.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHQKTPENYPNAGLTMYNCRND 61
DB 352 TPVQDCYHGDGQSYRGISSTVTGRTQCSWSSMTPHRHQKTPENYPNAGLTMYNCRND 411
QY 62 SGKQPMCYTTDPCVMEYCNLTQCSSETS 90
DB 412 ADKGPWCFTTDBSVMEYCNLKKCSGTEA 440

RESULT 13
US-09-131-995-1
Sequence 1, Application US/09131995
Patent No. 5972896
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 791 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
US-09-131-995-1

Query Match 78.5%; Score 423; DB 2; Length 791;
Best Local Similarity 78.7%; Pred. No. 2.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVODCYHGDGRSYRGISSTVTGRTCSQSSSMIPHHORTPENYNNAGLTENYCRNDP 61
DB 352 TPVODCYHGDGRSYRGISSTVTGRTCSQSSSMIPHHOKTPENYNNAGLTENYCRNDP 411

QY 62 SGKOPWCYTTDPCVRWEYCNLTQCSSETES 90
DB 412 ADKGPWCFTTDPSPVRWEYCNLKKCSGTEA 440

RESULT 14
US-08-832-087B-1
Sequence 1, Application US/08832087B
Patent No. 5981484
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087B
FILING DATE: 03-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 791 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
US-08-832-087B-1

Query Match 78.5%; Score 423; DB 2; Length 791;
Best Local Similarity 78.7%; Pred. No. 2.1e-37;
Matches 70; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 SPVODCYHGDGRSYRGISSTVTGRTCSQSSSMIPHHORTPENYNNAGLTENYCRNDP 61
DB 352 TPVODCYHGDGRSYRGISSTVTGRTCSQSSSMIPHHOKTPENYNNAGLTENYCRNDP 411

QY 62 SGKOPWCYTTDPCVRWEYCNLTQCSSETES 90
DB 412 ADKGPWCFTTDPSPVRWEYCNLKKCSGTEA 440

RESULT 15
US-08-851-350-1
Sequence 1, Application US/08851350
Patent No. 6057122
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
POLYNUCLEOTIDES ENCODING SAME AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,350
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:19:12 ; Search time 12.0451 Seconds
(without alignments)
710.580 Million cell updates/sec

Title: US-10-088-548-6

Perfect score: 523

Sequence: 1 VRQCYHNGNQSYRGFTFTV.....SIRWEXCNLTRCSDEGTGV 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 517 | 98.4 | 4548 | 1 S00657 | apoprotein(a) (EC |
| 2 | 476 | 91.4 | 1420 | 2 A32869 | apolipoprotein(a) |
| 3 | 444 | 84.9 | 810 | 1 PLHU | plasma (EC 3.4.21 |
| 4 | 433 | 82.8 | 810 | 2 B30848 | plasma (EC 3.4.21 |
| 5 | 415 | 79.3 | 812 | 1 PLBO | plasma (EC 3.4.21 |
| 6 | 413 | 79.0 | 120 | 2 E61545 | plasma (EC 3.4.21 |
| 7 | 407 | 77.8 | 123 | 2 C61545 | plasma (EC 3.4.21 |
| 8 | 401 | 76.7 | 790 | 1 PLRG | plasma (EC 3.4.21 |
| 9 | 400 | 76.5 | 812 | 1 PLMS | plasma (EC 3.4.21 |
| 10 | 392 | 75.0 | 810 | 2 B61545 | plasma (EC 3.4.21 |
| 11 | 388 | 74.2 | 460 | 2 A40522 | plasma (EC 3.4.21 |
| 12 | 381.5 | 72.9 | 169 | 2 A61545 | plasma (EC 3.4.21 |
| 13 | 380 | 72.7 | 455 | 2 A61545 | plasma (EC 3.4.21 |
| 14 | 354 | 67.7 | 89 | 2 A60140 | plasma (EC 3.4.21 |
| 15 | 303 | 57.9 | 2869 | 2 T18518 | apolipoprotein(a) |
| 16 | 272.5 | 52.1 | 716 | 1 A40332 | macrophage-stimula |
| 17 | 269 | 51.4 | 728 | 1 JH0579 | macrophage-stimula |
| 18 | 268.5 | 51.3 | 716 | 1 JCS061 | macrophage-stimula |
| 19 | 263 | 50.3 | 728 | 1 A35644 | macrophage-stimula |
| 20 | 263 | 50.3 | 728 | 1 A60185 | macrophage-stimula |
| 21 | 247.5 | 47.3 | 711 | 1 A47136 | macrophage-stimula |
| 22 | 246.5 | 47.1 | 710 | 1 I51285 | macrophage-stimula |
| 23 | 242 | 46.3 | 411 | 2 I51285 | macrophage-stimula |
| 24 | 237.5 | 45.4 | 946 | 1 A47299 | macrophage-stimula |
| 25 | 216.5 | 41.4 | 943 | 2 B45082 | macrophage-stimula |
| 26 | 205 | 39.2 | 336 | 2 S33879 | macrophage-stimula |
| 27 | 204.5 | 39.1 | 622 | 1 TBHU | macrophage-stimula |
| 28 | 204 | 39.0 | 625 | 1 TBBO | macrophage-stimula |
| 29 | 201.5 | 38.5 | 617 | 2 S10511 | macrophage-stimula |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 199.5 | 38.1 | 618 | 2 A35827 | chrombin (EC 3.4.2 |
| 31 | 193.5 | 37.0 | 603 | 2 S28941 | coagulation factor |
| 32 | 191.5 | 36.6 | 937 | 2 A45082 | neurotrophic recep |
| 33 | 189.5 | 36.2 | 560 | 1 UC4795 | plasma hyaluronan |
| 34 | 189 | 36.1 | 562 | 1 UKHUT | coagulation factor |
| 35 | 188.5 | 36.0 | 559 | 2 JCS878 | plasma hyaluronan |
| 36 | 174.5 | 33.4 | 558 | 2 JCS878 | coagulation factor |
| 37 | 173 | 33.1 | 559 | 1 A35029 | t-plasminogen acti |
| 38 | 173 | 33.1 | 559 | 1 A29941 | t-plasminogen acti |
| 39 | 171.5 | 32.8 | 432 | 1 S18932 | u-plasminogen acti |
| 40 | 170 | 32.5 | 655 | 1 A46888 | hepatocyte growth |
| 41 | 166.5 | 31.8 | 433 | 2 S45281 | coagulation factor |
| 42 | 160 | 30.6 | 493 | 1 UKBAY | u-plasminogen acti |
| 43 | 159 | 30.4 | 431 | 2 JCS059 | t-plasminogen acti |
| 44 | 159 | 30.4 | 477 | 1 A34369 | t-plasminogen acti |
| 45 | 159 | 30.4 | 477 | 2 JCS059 | t-plasminogen acti |

ALIGNMENTS

RESULT 1
S00657
apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N:Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 08-Dec-2000
C:Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65266
R:McLean, J.W.; Tomlinson, U.E.; Kuang, W.J.; Eaton, D.V.; Chen, E.Y.; Fless, G.M.; Scam
Nature 330, 132-137, 1987
A>Title: CDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A:Reference number: S00657; MUID:88039109; PMID:3670400
A:Accession: S00657
A:Molecule type: mRNA
A:Residues: 1-4548 <MCL>
A:Cross-references: GB:X06290; EMBL:X06696; NID:928619; PIDN:CAA29618.1; PID:928620
R:Eaton, D.V.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A>Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to
A:Reference number: A28017; MUID:87204109; PMID:3472206
A:Accession: A28017
A:Molecule type: Protein
A:Residues: 20-21, 'P', 23-34, 177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200/292-314, 'W', 316-3
X', 4396-4401 <EXT>
R:Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meier, K.; Schwartz,
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A>Title: 5' control regions of the apolipoprotein(a) gene and members of the related p
A:Reference number: A47277; MUID:93165698; PMID:7679504
A:Accession: A47277
A:Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:L07899; NID:9967973; PID:9967974
R:Magariel, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Se
Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A>Title: Characterization by yeast artificial chromosome cloning of the linked apolip
A:Reference number: A47233; MUID:93087573; PMID:1454851
A:Accession: A47233
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:M00078; NID:9178786; PIDN:AAA5547.1; PID:9553188
A:Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: A47233
A:Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:M00079; NID:9178784; PIDN:AAA5546.1; PID:9553187
R:Richiome, A
Biochemistry 31, 3113-3118, 1992
A>Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associ
A:Reference number: I52415; MUID:92207924; PMID:11554698
A:Accession: I52415

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <RB3>
 A:Cross-references: GB:M68677; NID:g178780; PIDN:AA89909.1; PID:g553185
 A:Note: apo(a) gene 1 (nomenclature of reference 152415)
 A:Accession: 165286
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <RB4>
 A:Cross-references: GB:M68678; NID:g178782; PIDN:AA51749.1; PID:g553186
 C:Genetics:
 A:Gene: GDB:LP4
 A:Cross-references: GDB:120699; OMIM:152200
 A:Map position: 6q25-6q27
 A:Note: several genes closely linked on chromosome 6 are identical in the first coding
 rs of kringle repeats
 C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
 C:Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
 F:1-19/Domains: signal sequence #status predicted <SIG>
 F:20-4548/Product: apolipoprotein(a) #status experimental <MAT>
 F:28-105/Domains: kringle homology <KR1>
 F:142-219/Domains: kringle homology <KR2>
 F:256-333/Domains: kringle homology <KR3>
 F:370-447/Domains: kringle homology <KR4>
 F:484-561/Domains: kringle homology <KR5>
 F:598-675/Domains: kringle homology <KR6>
 F:712-789/Domains: kringle homology <KR7>
 F:826-903/Domains: kringle homology <KR8>
 F:940-1017/Domains: kringle homology <KR9>
 F:1054-1131/Domains: kringle homology <KR10>
 F:1168-1245/Domains: kringle homology <KR11>
 F:1282-1359/Domains: kringle homology <KR12>
 F:1396-1473/Domains: kringle homology <KR13>
 F:1510-1587/Domains: kringle homology <KR14>
 F:1624-1701/Domains: kringle homology <KR15>
 F:1738-1815/Domains: kringle homology <KR16>
 F:1852-1929/Domains: kringle homology <KR17>
 F:1966-2043/Domains: kringle homology <KR18>
 F:2080-2157/Domains: kringle homology <KR19>
 F:2194-2271/Domains: kringle homology <KR20>
 F:2308-2385/Domains: kringle homology <KR21>
 F:2422-2499/Domains: kringle homology <KR22>
 F:2535-2613/Domains: kringle homology <KR23>
 F:2650-2727/Domains: kringle homology <KR24>
 F:2764-2841/Domains: kringle homology <KR25>
 F:2878-2955/Domains: kringle homology <KR26>
 F:2992-3069/Domains: kringle homology <KR27>
 F:3106-3183/Domains: kringle homology <KR28>
 F:3320-3297/Domains: kringle homology <KR29>
 F:3334-3411/Domains: kringle homology <KR30>
 F:3448-3525/Domains: kringle homology <KR31>
 F:3562-3639/Domains: kringle homology <KR32>
 F:3676-3753/Domains: kringle homology <KR33>
 F:3782-3859/Domains: kringle homology <KR34>
 F:3896-3973/Domains: kringle homology <KR35>
 F:4010-4087/Domains: kringle homology <KR36>
 F:4124-4201/Domains: kringle homology <KR37>
 F:4228-4307/Domains: kringle homology <KR38>
 F:4328-4541/Domains: trypsin homology <TRY>

Query Match 98.9%; Score 517; DB 1; Length 4548;
 Best Local Similarity 98.9%; Pred. No. 2,2e+44;
 Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRQCYHNGSGSYRGFTSTVTGRTCSWSMTPHRHQRTPEYNDGLTMNYCNPDADT 60
 DB 4121 VRQCYHNGSGSYRGFTSTVTGRTCSWSMTPHRHQRTPEYNDGLTMNYCNPDADT 4180

QY 61 GPCFETDPSIRWEYCNLTRCSDEGTIV 89
 DB 4181 GPCFETDPSIRWEYCNLTRCSDEGTIV 4209

RESULT 2
 A32869
 A:apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 22-Jun-1999
 C:Accession: A32869; A30848
 R:Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
 J. Biol. Chem. 264, 5957-5965, 1989
 A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis
 A:Reference number: A32869; MUID:89174660; PMID:2925643
 A:Accession: A32869
 A:Molecule type: mRNA
 A:Residues: 1-1420 <TOM>
 A:Cross-references: GB:J04635; NID:g342072; PIDN:AA36833.1; PID:g342073
 C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
 C:Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
 F:50-127/Domains: kringle homology <KR1>
 F:164-241/Domains: kringle homology <KR2>
 F:278-355/Domains: kringle homology <KR3>
 F:392-469/Domains: kringle homology <KR4>
 F:506-583/Domains: kringle homology <KR5>
 F:620-697/Domains: kringle homology <KR6>
 F:726-803/Domains: kringle homology <KR7>
 F:840-917/Domains: kringle homology <KR8>
 F:954-1031/Domains: kringle homology <KR9>
 F:1068-1145/Domains: kringle homology <KR10>
 F:1191-1413/Domains: trypsin homology <TRY>

Query Match 91.4%; Score 478; DB 2; Length 1420;
 Best Local Similarity 91.0%; Pred. No. 6.7e+41;
 Matches 81; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 VRQCYHNGSGSYRGFTSTVTGRTCSWSMTPHRHQRTPEYNDGLTMNYCNPDADT 60
 DB 1065 VRQCYHNGSGSYRGFTSTVTGRTCSWSMTPHRHQRTPEYNDGLTMNYCNPDADT 1124

QY 61 GPCFETDPSIRWEYCNLTRCSDEGTIV 89
 DB 1125 GPCFETDPSIRWEYCNLTRCSDEGTIV 1153

RESULT 3
 PLNU
 A:plasmin (EC 3.4.21.7) precursor [validated] - human
 N:Alternate names: plasminogen precursor [msnomen]
 N:Contents: angiotensin; microplasmin; plasminogen
 C:Species: Homo sapiens (man)
 C:Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000
 C:Accession: A35229; 152242; A26646; 162738; 184609; 503735; A00929; A04627; A04625; A046
 J. Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
 J. Biol. Chem. 265, 6104-6111, 1990
 A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibr
 A:Reference number: A35229; MUID:90202879; PMID:2318648
 A:Accession: A35229
 A:Molecule type: DNA
 A:Residues: 1-810 <BET>
 A:Cross-references: GB:J05286; GB:M34276; NID:g190064; PIDN:AAA60113.1; PID:g387026
 R:Margaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Tai
 Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
 A:Title: Definition of the transfection initiation site of human plasminogen gene in 11v
 A:Reference number: 152242; MUID:91097523; PMID:2268308
 A:Accession: 152242
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <MAL>
 A:Cross-references: GB:M62890; NID:g190092; PIDN:AA36454.1; PID:g553613
 R:Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
 FEBS Lett. 213, 254-260, 1987
 A:Title: Molecular cloning and characterization of a full-length cDNA clone for human pl
 A:Reference number: A26646; MUID:87162490; PMID:3030813
 A:Accession: A26646
 A:Molecule type: mRNA

A:Residues: 1-471, 'D', 473-810 <FOR>
 A:Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
 A:Experimental source: liver
 R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
 Biochemistry 23, 4243-4250, 1984
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and
 A:Reference number: 145961; PMID:85023311; PMID:6148961
 A:Accession: 162738
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 292-471, 'D', 473-810 <MAL2>
 A:Cross-references: GB:X02922; NID:g190112; PIDN:AAA60124.1; PID:g387031
 A:Accession: 184609
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 367-419 <MAL3>
 A:Cross-references: GB:X02921; NID:g190110; PIDN:AAA60123.1; PID:g190111
 R:Brundish, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
 Eur. J. Biochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
 A:Reference number: S03735; PMID:81212097; PMID:7238497
 A:Accession: S03735
 A:Molecule type: protein
 A:Residues: 20-71, 'E', 73-76 <BRU>
 R:Sortrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
 submitted to the Atlas, July 1977
 A:Reference number: A00929
 A:Accession: A00929
 A:Molecule type: protein
 A:Residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>
 R:Wiman, B.
 Eur. J. Biochem. 76, 129-137, 1977
 A:Title: Primary structure of the B-chain of human plasmin.
 A:Reference number: A04627; PMID:77225245; PMID:142009
 A:Accession: A04627
 A:Molecule type: protein
 A:Residues: 581-810 <W1>
 R:Wiman, B.; Wallen, P.
 Eur. J. Biochem. 50, 489-494, 1975
 A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human pl
 A:Reference number: A04625; PMID:75093329; PMID:122932
 A:Accession: A04625
 A:Molecule type: protein
 A:Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <W12>
 R:Wiman, B.; Wallen, P.
 Eur. J. Biochem. 58, 539-547, 1975
 A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha
 A:Reference number: A04626; PMID:76043692; PMID:126863
 A:Accession: A04626
 A:Molecule type: protein
 A:Residues: 483-507, 'E', 509-604 <W13>
 R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
 J. Biol. Chem. 248, 1631-1633, 1973
 A:Title: The primary structure of human plasminogen. II. The histidine loop of human pl
 A:Reference number: A92125; PMID:73149248; PMID:4694729
 A:Contents: annotation; active site
 R:Grozkopf, W.R.; Summaria, L.; Robbins, K.C.
 J. Biol. Chem. 244, 3590-3597, 1969
 A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
 A:Reference number: A92048; PMID:69234739; PMID:4420117
 A:Contents: annotation; active site
 R:Trexler, M.; Valli, Z.; Patchy, L.
 J. Biol. Chem. 257, 7401-7406, 1982
 A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
 A:Reference number: A92382; PMID:6213905; PMID:6919539
 A:Contents: annotation; omega-aminocarboxylic acid binding sites
 R:Valli, Z.; Patchy, L.
 J. Biol. Chem. 259, 13690-13694, 1984
 A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
 A:Reference number: A92458; PMID:85054794; PMID:6094526
 A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
 R:Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.;

J. Biol. Chem. 271, 29461-29467, 1996
 A:Title: Kringle domains of human angiotensin. Characterization of the anti-proliferative
 A:Reference number: A58811; PMID:97067211; PMID:8910613
 A:Contents: annotation
 R:Julien, H.R.; Uguw, F.; Bini, A.; Collen, D.
 Biochemistry 37, 4699-4702, 1998
 A:Title: Generation of an angiotensin-like fragment from plasminogen by streptolysin-1 (M
 A:Reference number: A58812; PMID:9548733; PMID:9548733
 A:Contents: annotation
 R:Tulinsky, A.; Mulichak, A.M.
 submitted to the Brookhaven Protein Data Bank, July 1991
 A:Reference number: A51341; PDB:1PK4
 A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
 R:Tulinsky, A.; Wu, T.P.
 submitted to the Brookhaven Protein Data Bank, July 1991
 A:Reference number: A51488; PDB:2PK4
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
 R:Wu, T.P.; Tulinsky, A.
 submitted to the Brookhaven Protein Data Bank, August 1993
 A:Reference number: A51911; PDB:1PKR
 A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
 R:Padmanabhan, K.; Tulinsky, A.
 submitted to the Brookhaven Protein Data Bank, April 1994
 A:Reference number: A52408; PDB:1PKM
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
 R:Tulinsky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995
 A:Reference number: A55244; PDB:1CEA
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
 R:Tulinsky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995
 A:Reference number: A55245; PDB:1CEB
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
 R:Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
 Biochemistry 30, 10576-10588, 1991
 A:Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 A
 A:Reference number: A58819; PMID:92031502; PMID:1657148
 A:Contents: annotation
 R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
 Biochemistry 30, 10589-10594, 1991
 A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin
 A:Reference number: A58818; PMID:92031503; PMID:1657149
 A:Contents: annotation
 R:De Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.I
 Biochemistry 31, 270-279, 1992
 A:Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4
 A:Reference number: A39483; PMID:92118803; PMID:1310033
 A:Contents: annotation; X-ray crystallography, 2.4 angstroms
 R:Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
 submitted to the Brookhaven Protein Data Bank, June 1995
 A:Reference number: A65980; PDB:1KRN
 A:Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
 R:Rejzante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A65803; PDB:1HRJ
 A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
 R:Rejzante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A65804; PDB:1HRK
 A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
 R:Rejzante, M.; Llinas, M.
 Eur. J. Biochem. 221, 927-937, 1994
 A:Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
 A:Reference number: A43645; PMID:94237157; PMID:8181475
 A:Contents: annotation; conformation by (1)H-NMR, residues 96-184
 R:Rejzante, M.; Llinas, M.
 Eur. J. Biochem. 221, 939-949, 1994
 A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminoge
 A:Reference number: A58817; PMID:94237158; PMID:8181476
 A:Contents: annotation; conformation by (1)H-NMR
 C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many oth
 C:Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU ar
 d PIR:FGHUGB).

F:315/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:365/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 79.3%; Score 415; DB 1; Length 812;
Best Local Similarity 79.5%; Pred. No. 1,1e-34;
Matches 66; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 ROCYHNGOSYRGFTSTVTGRTCCQSWSMTPRHQRTPENYNDGLTMNYCRNPADATG 61
DB 382 QDCYHNGOSYRGFTSTVTGRTCCQSWSMTPRHQRTPENYNDGLTMNYCRNPADATG 441
QY 62 PWCFTTDPISIRWEXCNLTRCSDT 84
DB 442 PWCYTTDPRIWRWFCNLKCKSET 464

RESULT 6

plasma (EC 3.4.21.7) precursor - dog (fragments)
N:Alternate names: plasminogen
C:Species: Canis lupus familiaris (dog)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
C:Accession: B61545
R:Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A:Title: Structural aspects of the plasminogen of various species.
A:Reference number: A61545; MUID:8905015; PMID:3168975
A:Accession: B61545
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-120 <SCH>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: hydrolase; serine proteinase
F:37-114/Domain: kringle homology <KR4>

Query Match 79.0%; Score 413; DB 2; Length 120;
Best Local Similarity 74.7%; Pred. No. 2,6e-35;
Matches 65; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VROCYHNGOSYRGFTSTVTGRTCCQSWSMTPRHQRTPENYNDGLTMNYCRNPADATG 60
DB 34 VORCYHNGOSYRGFTSTVTGRTCCQSWSMTPRHQRTPENYNDGLTMNYCRNPADATG 93
QY 61 GPWCFTTDPISIRWEXCNLTRCSDT 87
DB 94 SPWCYTTDPRIWRWFCNLKCKSET 120

RESULT 7

plasma (EC 3.4.21.7) precursor - goat (fragments)
N:Alternate names: plasminogen
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
C:Accession: C61545
R:Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A:Title: Structural aspects of the plasminogen of various species.
A:Reference number: A61545; MUID:8905015; PMID:3168975
A:Accession: C61545
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-123 <SCH>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: hydrolase; serine proteinase
F:41-118/Domain: kringle homology <KR4>

Query Match 77.8%; Score 407; DB 2; Length 123;
Best Local Similarity 79.3%; Pred. No. 1,1e-34;
Matches 65; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 ROCYHNGOSYRGFTSTVTGRTCCQSWSMTPRHQRTPENYNDGLTMNYCRNPADATG 61

DB 39 QDCYHNGOSYRGFTSTVTGRTCCQSWSMTPRHQRTPESYPNAGLTMYCRNPADATG 98

QY 62 PWCFTTDPISIRWEXCNLTRCSD 83
DB 99 PWCYTTDPRIWRWFCNLKCKSET 120

RESULT 8

plasma (EC 3.4.21.7) precursor - pig (fragment)
N:Alternate names: plasminogen
N:Contains: miniplasminogen
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C:Accession: S03733; S03737; A25834
R:Schaller, J.; Marti, T.; Koessele, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A:Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the cat
A:Reference number: S03733
A:Accession: S03733
A:Molecule type: protein
A:Residues: 1-560 <SCH>
R:Brundish, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human, l
A:Reference number: S03735; MUID:81212097; PMID:7238497
A:Accession: S03737
A:Molecule type: protein
A:Residues: 1-57 <BRU>
R:Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A:Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A:Reference number: A25834; MUID:85203907; PMID:3846533
A:Accession: A25834
A:Molecule type: protein
A:Residues: 450-790 <MAR>
C:Function:

A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the graafian follicle; also activates the urokinase-type plasminogen activator
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology; C:Keywords: fibrinolysis; glycoprotein; hydrolyase; kidney; kringle; plasma; serine protease
F:1-790/Product: plasminogen #status predicted <PRO>
F:1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
F:78-77/Domain: activation peptide #status predicted <AP>
F:78-560/Product: plasmin chain A #status predicted <ACH>
F:84-162/Domain: kringle homology <KR1>
F:166-243/Domain: kringle homology <KR2>
F:256-333/Domain: kringle homology <KR3>
F:358-435/Domain: kringle homology <KR4>
F:450-790/Product: miniplasminogen #status experimental <MTN>
F:461-540/Domain: kringle homology <KR5>
F:561-790/Product: plasmin chain B #status experimental <BCH>
F:561-783/Domain: trypsin homology <TRY>
F:30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305-bonds: #status predicted
F:602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 76.7%; Score 401; DB 1; Length 790;
Best Local Similarity 73.6%; Pred. No. 2,8e-33;
Matches 64; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 ROCYHNGOSYRGFTSTVTGRTCCQSWSMTPRHQRTPENYNDGLTMNYCRNPADATG 61
DB 356 QDCYHNGOSYRGFTSTVTGRTCCQSWSMTPRHQRTPENYNDGLTMNYCRNPADATG 415
QY 62 PWCFTTDPISIRWEXCNLTRCSDT 88
DB 416 PWCYTTDPRIWRWFCNLKCKSET 442

RESULT 9

PLMS
 Plasmin (EC 3.4.21.7) precursor - mouse
 N/contains: angiotensin; plasminogen
 C/Species: Mus musculus (house mouse)
 C/Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
 C/Accession: A38514; S48202; S48203
 R/Begun, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
 Genomics 8, 49-61, 1990
 A/Title: Characterization of the cDNA coding for mouse plasminogen and localization of
 A/Reference number: A38514; MUID:91184812; PMID:2081600
 A/Accession: A38514
 A/Molecule type: mRNA
 A/Residues: 1-812 <DEG>
 A/Cross-references: GB:J04766; NID:G200402; PIDN:AAA50168.1; PID:G200403
 R/Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
 Eur. J. Biochem. 224, 863-871, 1994
 A/Title: Characterization of the murine plasma fibrinolytic system.
 A/Reference number: S48202; MUID:95010076; PMID:7523120
 A/Accession: S48202
 A/Molecule type: protein
 A/Residues: 20-25 <LIJ>
 A/Molecule type: protein
 A/Residues: 548203
 A/Comment: Plasminogen is synthesized by the kidney and is present in plasma and many of
 C/Comment: plasminogen is converted into plasmin by plasminogen activators, both plasmin
 e inhibitor, the activation involves also removal of the inhibitor, the activat
 C/Comment: Streptolysin 1 (see PIR:KCMS51) acts on plasminogen to produce angiotensin. To
 eful in treating solid tumors.
 C/Function:
 A/Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 ne the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A/Pathway: fibrinolysis
 C/Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology
 C/Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
 F/1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-812/Product: plasminogen #status predicted <PRO>
 F/20-96/Domain: activation peptide #status predicted <APT>
 F/79-466/Product: angiotensin #status predicted <AST>
 F/97-561,582-812/Product: plasmin #status predicted <MAT>
 F/97-581/Domain: chain A #status predicted <ACH>
 F/103-181/Domain: kringe homology <KR1>
 F/185-262/Domain: kringe homology <KR2>
 F/275-352/Domain: kringe homology <KR3>
 F/377-454/Domain: kringe homology <KR4>
 F/481-560/Domain: kringe homology <KR5>
 F/582-812/Domain: chain B #status predicted <BCH>
 F/582-805/Domain: trypsin homology <TRY>
 F/49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds; #status predicted
 F/78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
 F/136,308/Binding site: carboxylate (Asn) (covalent) #status predicted
 F/466-467/Cleavage site: Tyr-Val (stromelysin 1) #status predicted
 F/581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
 F/624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 76.5%; Score 400; DB 1; Length 812;
 Best Local Similarity 70.8%; Pred. No. 3,7e-33;
 Matches 63; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 1 VROCYHNGGSGYRGFTSTVTGRTGQSSGSMTPRHQRTPENYNDGLTMNYCRNPADT 60
 DB 374 VQECYQSGGSGYRGFTSTVTGRTGQSSGSMAMPPIRHSHKTPENPDAGLENNYCRNPDGDK 433

QY 61 GPMCFITDPSIRWEYCNLTRCSPTDETVV 89
 DB 434 GPMCFITDPSIRWEYCNLTRCSPTDETVV 462

RESULT 10
 146260

plasmin (EC 3.4.21.7) precursor - western European hedgehog
 C/Species: Erinaceus europaeus (western European hedgehog)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C/Accession: I46260
 R/Law, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong,
 J. Biol. Chem. 270, 24004-24009, 1995
 A/Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprote
 A/Reference number: I46259; MUID:96025778; PMID:7592597
 A/Accession: I46260
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-810 <LAW>
 A/Cross-references: EMBL:U33171; NID:G1046360; PID:G1046361
 C/Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology;
 C/Keywords: hydrolase; serine protease
 F/1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 F/103-181/Domain: kringe homology <KR1>
 F/185-262/Domain: kringe homology <KR2>
 F/275-352/Domain: kringe homology <KR3>
 F/379-456/Domain: kringe homology <KR4>
 F/482-561/Domain: kringe homology <KR5>
 F/582-803/Domain: trypsin homology <TRY>

Query Match 75.0%; Score 392; DB 2; Length 810;
 Best Local Similarity 71.8%; Pred. No. 2.4e-32;
 Matches 61; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 VROCYHNGGSGYRGFTSTVTGRTGQSSGSMTPRHQRTPENYNDGLTMNYCRNPADT 60
 DB 376 VQECYQSGGSGYRGFTSTVTGRTGQSSGSMTPRHSHKTPENPDADLENNYCRNPDGDK 435

QY 61 GPMCFITDPSIRWEYCNLTRCSPTDETVV 85
 DB 436 GPMCFITDPSIRWEYCNLTRCSPTDETVV 460

RESULT 11
 B61545
 Plasmin (EC 3.4.21.7) precursor - sheep (fragments)
 N/Alternate names: plasminogen
 C/Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
 C/Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999
 C/Accession: B61545; S28200
 R/Schaller, J.; Rickli, E.E.
 Enzyme 40, 63-69, 1988
 A/Title: Structural aspects of the plasminogen of various species.
 A/Reference number: A61545; MUID:89005015; PMID:3168975
 A/Accession: B61545
 A/Molecule type: protein
 A/Residues: 1-37,38-117 <SCH>
 R/Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
 Protein Seq. Data Anal. 5, 21-25, 1992
 A/Title: Complete amino acid sequence of ovine miniplasminogen.
 A/Reference number: S28200; MUID:93149995; PMID:1492092
 A/Accession: S28200
 A/Molecule type: protein
 A/Residues: 118-460 <SC2>
 C/Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology;
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringe; plasma; serine proteinase;
 F/1-37,38-117,118-460/Product: plasminogen (fragments) #status experimental <PRO>
 F/1-37/Domain: activation peptide (fragment) #status experimental <APT>
 F/38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT>
 F/41-118/Domain: kringe homology <KR4>
 F/118-60/Product: miniplasminogen #status experimental <MIN>
 F/132-211/Domain: kringe homology <KR5>
 F/226-460/Domain: plasmin chain B #status experimental <BCH>
 F/231-453/Domain: trypsin homology <TRY>
 F/272,315,410/Active site: His, Asp, Ser #status predicted

Query Match 74.2%; Score 388; DB 2; Length 460;
 Best Local Similarity 78.5%; Pred. No. 3.5e-32;
 Matches 62; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

[illegible]

F:126-205/Domain: kringle homology <KR5>
F:226-455/Domain: plasmin chain B #status experimental <BCH>
F:226-448/Domain: trypsin homology <TRY>
F:267,310,405/Active site: His, Asp, Ser #status predicted

Query Match 72.7%; Score 380; DB 2; Length 455;
Best Local Similarity 72.6%; Pred. No. 2,3e-31;
Matches 61; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

OY 1 VRCYTHNGSGSYRGFTSTVTYGRTCOSWSMTPHRHQRTPEYNDGLTMNYCRNPADDT 60
Db 34 VQDCYQDGBSEYRGFTSTVTYGRTCOSWSMTPHRHQRTPEYNDGLTMNYCRNPADDT 93
OY 61 GPMCFETDPSIRMEYCNLTTRCSDT 84
Db 94 GPMCFETDPSIRMEYCNLTTRCSDT 117

RESULT 14
A60140
Plasmin (EC 3.4.21.7) precursor - chicken (fragment)
N:Alternate names: plasminogen
C:Species: Gallus gallus (chicken)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
C:Accession: A60140
R:Gene(s), M., Patchy, L.
Biochim. Biophys. Acta 832, 326-330, 1985
A:Title: The kringle 4 domain of chicken plasminogen.
A:Reference number: A60140; MUID:86077796; PMID:4074753
A:Accession: A60140
A:Molecule type: protein
A:Residues: 1-89 <GR>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
F:6-83/Domain: kringle homology <KR>
F:6-83,27-66,55-76/Disulfide bonds: #status predicted
F:39/Binding site: carbohydrate (Aen) (covalent) #status experimental

Query Match 67.7%; Score 354; DB 2; Length 89;
Best Local Similarity 67.9%; Pred. No. 2,1e-29;
Matches 55; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

OY 3 OCYHNGSGSYRGFTSTVTYGRTCOSWSMTPHRHQRTPEYNDGLTMNYCRNPADDTGP 62
Db 5 ECYQNGSGSYRGFTSTVTYGRTCOSWSMTPHRHQRTPEYNDGLTMNYCRNPADDTGP 64
OY 63 WCFTTDPSPIRMEYCNLTTRCSD 83
Db 65 WCFTTDPSPIRMEYCNLTTRCSD 85

RESULT 15
T18518
Apolipoprotein(a) - western European hedgehog (fragment)
C:Species: Erinaceus europaeus (western European hedgehog)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C:Accession: T18518
R:Lawn, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.B.; Wade, D.P.; Byrne, C.D.; Fong, J. Biol. Chem. 270, 24004-24009, 1995
A:Title: The recurring evolution of lip(a): Insights from cloning of hedgehog apolipoprotein
A:Reference number: 146259; MUID:96025778; PMID:7592597
A:Accession: T18518
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2869 <LAW>
A:Cross-references: EMBL:U33170; NID:g1046358; PID:g1046359; PIDN:AA048522.1
A:Experimental source: liver
C:Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, contains apolipoprotein(a).

Query Match 57.9%; Score 303; DB 2; Length 2869;
Best Local Similarity 56.2%; Pred. No. 1,1e-22;
Matches 46; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

| | | | | | |
|----|------|------------------------------|-------------|--------------------|------|
| QY | 3 | OCVHNGOSYRGTFSTTVTGRTCOSWSMT | PHRHORTPENY | PNDGLTMNYCRUPADTGP | 62 |
| Db | 2776 | QCLKNGESTOGNISVTSGYTCORNEOT | PHRHARTPDNY | PCNLYGNYCRNPDGEVAP | 2835 |
| QY | 63 | WCFTDPSIRWEYCNLTRC | 81 | | |
| Db | 2836 | WCYTNSAVRWEYCSIPTC | 2854 | | |

Search completed: January 12, 2004, 17:26:24
 job time : 13.0451 secs

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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:17.22 ; Search time 7.69549 Seconds

(without alignments)
543.874 Million cell updates/sec

Title: US-10-088-548-6

Perfect score: 523

Sequence: 1 VRQCHNGNQSYRGFTSTV.....SIRWEXNLTGRCSDTEGTIV 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 517 | 98.9 | 4548 | 1 | APOA_HUMAN |
| 2 | 478 | 91.4 | 1420 | 1 | APOA_MACMU |
| 3 | 444 | 84.9 | 810 | 1 | PLMN_HUMAN |
| 4 | 433 | 82.8 | 810 | 1 | PLMN_MACMU |
| 5 | 435 | 79.3 | 812 | 1 | PLMN_BOVIN |
| 6 | 401 | 76.7 | 790 | 1 | PLMN_PIG |
| 7 | 400 | 76.5 | 812 | 1 | PLMN_MOUSE |
| 8 | 392 | 75.0 | 810 | 1 | PLMN_ERIEU |
| 9 | 381.5 | 72.9 | 169 | 1 | PLMN_RAT |
| 10 | 272.5 | 52.1 | 716 | 1 | HGF_MOUSE |
| 11 | 269 | 51.4 | 728 | 1 | HGF_HUMAN |
| 12 | 263 | 50.3 | 728 | 1 | HGF_MOUSE |
| 13 | 263 | 50.3 | 728 | 1 | HGF_RAT |
| 14 | 247.5 | 47.3 | 711 | 1 | HGFL_HUMAN |
| 15 | 234 | 44.7 | 343 | 1 | PLMN_SHEEP |
| 16 | 233 | 44.6 | 333 | 1 | PLMN_CANFA |
| 17 | 222 | 42.4 | 338 | 1 | PLMN_HORSE |
| 18 | 216.5 | 41.4 | 943 | 1 | ROR2_HUMAN |
| 19 | 208.5 | 39.9 | 944 | 1 | ROR2_MOUSE |
| 20 | 205 | 39.2 | 325 | 1 | PLMN_PETMA |
| 21 | 204.5 | 39.1 | 632 | 1 | THRB_HUMAN |
| 22 | 204 | 39.0 | 635 | 1 | THRB_BOVIN |
| 23 | 201.5 | 38.5 | 617 | 1 | THRB_RAT |
| 24 | 199.5 | 38.1 | 618 | 1 | THRB_MOUSE |
| 25 | 193.5 | 37.0 | 603 | 1 | FA12_CAVPO |
| 26 | 192.5 | 36.8 | 937 | 1 | ROR1_MOUSE |
| 27 | 191.5 | 36.6 | 937 | 1 | ROR1_HUMAN |
| 28 | 189 | 36.1 | 937 | 1 | TPA_HUMAN |
| 29 | 188.5 | 36.0 | 615 | 1 | FA12_HUMAN |
| 30 | 187.5 | 35.9 | 724 | 1 | ROR2_DROME |
| 31 | 182 | 34.8 | 566 | 1 | TPA_BOVIN |
| 32 | 174 | 33.3 | 653 | 1 | HGFA_MOUSE |
| 33 | 173 | 33.1 | 559 | 1 | TPA_MOUSE |

| | | | | | | | |
|----|-------|------|-----|---|------------|--------|-------------|
| 34 | 173 | 33.1 | 559 | 1 | TPA_RAT | P19637 | rattus norv |
| 35 | 171.5 | 32.8 | 432 | 1 | UROK_RAT | P29598 | rattus norv |
| 36 | 170 | 32.5 | 655 | 1 | HGFA_HUMAN | O04756 | homo sapien |
| 37 | 167.5 | 32.0 | 473 | 1 | KRM1_MOUSE | O99n43 | mus musculu |
| 38 | 167.5 | 32.0 | 473 | 1 | KRM1_RAT | O92484 | mus musculu |
| 39 | 166.5 | 31.8 | 593 | 1 | FA12_BOVIN | P98140 | bos taurus |
| 40 | 164.5 | 31.5 | 475 | 1 | KRM1_HUMAN | O96m08 | homo sapien |
| 41 | 163.5 | 31.3 | 452 | 1 | KRM1_XENLA | O90y90 | xenopus lae |
| 42 | 160 | 30.6 | 433 | 1 | UROK_PAPCY | P16227 | papio cynoc |
| 43 | 159 | 30.4 | 431 | 1 | URTB_DESRO | P98121 | desmodus ro |
| 44 | 159 | 30.4 | 462 | 1 | KRM2_HUMAN | O8ncw0 | homo sapien |
| 45 | 159 | 30.4 | 477 | 1 | URT2_DESRO | P15638 | desmodus ro |

ALIGNMENTS

RESULT 1

| ID | APOA_HUMAN | STANDARD | PRT | 4548 AA. |
|----|--|----------|-----|----------|
| AC | P08519 | | | |
| DT | 01-AUG-1988 (Rel. 08, Created) | | | |
| DT | 01-AUG-1988 (Rel. 08, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)). | | | |
| GN | LpA. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=88039109; PubMed=3670400; | | | |
| RA | McLean J.W., Tomlinson J.E., Kuang W.-J., Eaton D.L., Chen E.Y., | | | |
| RA | Fleiss G.M., Scam A.M., Lawn R.M.; | | | |
| RT | "cDNA sequence of human apolipoprotein(a) is homologous to | | | |
| RT | plasminogen."; | | | |
| RL | Nature 330:132-137(1987). | | | |
| RN | [2] | | | |
| RP | SERINE PROTEASE ACTIVITY. | | | |
| RX | MEDLINE=90076123; PubMed=2531657; | | | |
| RA | Salonen E.-M., Jauhainen M., Zairi L., Vaheri A., Ehnholm C.; | | | |
| RT | "Lipoprotein(a) binds to fibronectin and has serine proteinase | | | |
| RT | activity capable of cleaving it."; | | | |
| RL | EMBO J. 8:4035-4040(1989). | | | |
| RN | [3] | | | |
| RP | REVIEW. | | | |
| RX | MEDLINE=90049223; PubMed=2530631; | | | |
| RA | Utermann G.; | | | |
| RT | "The mysteries of lipoprotein(a)."; | | | |
| RL | Science 246:904-910(1989). | | | |
| RN | [4] | | | |
| RP | CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS. | | | |
| RX | MEDLINE=21303595; PubMed=11294842; | | | |
| RA | Garner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.; | | | |
| RT | "Structural elucidation of the N- and O-glycans in conferring protease | | | |
| RT | apolipoprotein(a): role of O-glycans in conferring protease | | | |
| RT | resistance."; | | | |
| RL | J. Biol. Chem. 276:22200-22208(2001). | | | |
| RN | [5] | | | |
| RP | X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208. | | | |
| RX | MEDLINE=96217891; PubMed=8642595; | | | |
| RA | Mikol V., Lograsse P.V., Beutcher B.R.; | | | |
| RT | "Crystal structures of apolipoprotein(a) kringle IV3 free and | | | |
| RT | complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic | | | |
| RT | acid: existence of novel and expected binding modes."; | | | |
| RL | J. Mol. Biol. 256:751-761(1996). | | | |
| RN | [6] | | | |
| RP | VARIANT ARG-4193. | | | |
| RX | MEDLINE=95002201; PubMed=7918682; | | | |
| RA | Scam A.M., Pfaffinger D., Lee J.C., Himan J.; | | | |
| RT | "A single point mutation (Trp72->Arg) in human apo(a) kringle 4-37 | | | |
| RT | associated with a lysine binding defect in Lp(a)."; | | | |

| | |
|----|--|
| CC | Bloodm; Biophys. Acta 1227:41-45(1994). |
| CC | - FUNCTION: Apo(a) is the main constituent of lipoprotein(a) |
| CC | (Lp(a)). It has serine proteinase activity and is able of |
| CC | autohydrolysis. Inhibits tissue-type plasminogen activator 1. |
| CC | Lp(a) may be a ligand for megalin/GP 330. |
| CC | - SUBUNIT: disulfide-linked to apo-B100. Binds to fibronectin and |
| CC | decorin. |
| CC | - PTM: N- and O-glycosylated. The N-glycans are complex biantennary |
| CC | structures present in either a mono- or disialylated state. The |
| CC | O-glycans are mostly (80%) represented by the monosialylated core |
| CC | type-I structure, NeuNacalpha2-3Galbeta1-3GlcNAc, with smaller |
| CC | amounts of disialylated and non-sialylated O-glycans also |
| CC | detected. |
| CC | - DISEASE: Elevated plasma concentrations of apo(a) and its |
| CC | naturally occurring proteolytic fragments are correlated with |
| CC | atherosclerosis. Homology with plasminogen kringle IV and V is |
| CC | thought to underlie the atherogenicity of the protein, because the |
| CC | fragments are competing with plasminogen for fibrin(ogen) binding. |
| CC | - MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved, |
| CC | leading to the formation of the so called mini-Lp(a). Apo(a) may |
| CC | promote thromboaggregation in atherosclerotic lesions, where they may |
| CC | promote proteolysis. O-glycosylation may limit the extent of |
| CC | proteolytic fragmentation. |
| CC | - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY. |
| CC | - SIMILARITY: Contains 36 kringle domains. |
| CC | ----- |
| CC | This SWISS-PROT entry is copyrighted. It is produced through a collaboration |
| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation - |
| CC | the European Bioinformatics Institute. There are no restrictions on its |
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| CC | modified and this statement is not removed. Usage by and for commercial |
| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce |
| CC | or send an email to license@isb-sib.ch). |
| CC | ----- |
| DR | EMBL; X06290; CAA29618.1; -- |
| DR | PIR; S00657; S00657. |
| DR | PDB; 1I7I; 13-JUN-01. |
| DR | PDB; 1JEN; 28-JUN-02. |
| DR | PDB; 1KIV; 18-MAY-99. |
| DR | PDB; 3KIV; 18-MAY-99. |
| DR | PDB; 4KIV; 18-MAY-99. |
| DR | MEROPS; S01_226; -- |
| DR | GeneW; HGNC:6667; LPA. |
| DR | MM; 152200; -- |
| DR | GO; GO:0004866; F:endopeptidase inhibitor activity; TAS. |
| DR | GO; GO:0008015; P:circulation; TAS. |
| DR | GO; GO:0009405; P:pathogenesis; TAS. |
| DR | InterPro; IPR001314; Chymotrypsin. |
| DR | InterPro; IPR000001; Kringle. |
| DR | InterPro; IPR001254; Ser_protease_Try. |
| DR | Pfam; PF00051; Kringle; 38. |
| DR | Pfam; PF00089; trypsin; 1. |
| DR | PRINTS; PR00722; CHYMOTRYPSIN. |
| DR | PRINTS; PR00018; KRINGLE. |
| DR | ProDom; PD000395; Kringle; 38. |
| DR | SMART; SM00130; KR; 38. |
| DR | SMART; SM00020; TRY_PPC; 1. |
| DR | PROSITE; PS00021; KRINGLE_1; 38. |
| DR | PROSITE; PSS0070; KRINGLE_2; 38. |
| DR | PROSITE; PSS0240; TRYPsin_DOM; 1. |
| DR | PROSITE; PS00134; TRYPsin_HIS; 1. |
| DR | PROSITE; PS00133; TRYPsin_SER; 1. |
| KW | Hydrolase; Serine protease; Lipid transport; Plasma; Glycoprotein; |
| KW | Kringle; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure. |
| FT | SIGNAL 1 19 |
| FT | CHAIN 20 4548 APOLIPOPROTEIN(A). |
| FT | DOMAIN 20 130 KRINGLE TYPE IV, 1. |
| FT | DOMAIN 131 244 KRINGLE TYPE IV, 2. |
| FT | DOMAIN 245 358 KRINGLE TYPE IV, 3. |
| FT | DOMAIN 359 472 KRINGLE TYPE IV, 4. |
| FT | DOMAIN 473 586 KRINGLE TYPE IV, 5. |
| FT | DOMAIN 587 700 KRINGLE TYPE IV, 6. |
| FT | DOMAIN 701 814 KRINGLE TYPE IV, 7. |

| FT | DOMAIN | 815 | 928 | KRINGLE TYPE IV, 8. |
|-------------|---|--|--------------------|--|
| FT | DOMAIN | 929 | 1042 | KRINGLE TYPE IV, 9. |
| FT | DOMAIN | 1043 | 1156 | KRINGLE TYPE IV, 10. |
| FT | DOMAIN | 1157 | 1270 | KRINGLE TYPE IV, 11. |
| FT | DOMAIN | 1271 | 1384 | KRINGLE TYPE IV, 12. |
| FT | DOMAIN | 1385 | 1498 | KRINGLE TYPE IV, 13. |
| FT | DOMAIN | 1499 | 1612 | KRINGLE TYPE IV, 14. |
| FT | DOMAIN | 1613 | 1726 | KRINGLE TYPE IV, 15. |
| FT | DOMAIN | 1727 | 1840 | KRINGLE TYPE IV, 16. |
| FT | DOMAIN | 1841 | 1954 | KRINGLE TYPE IV, 17. |
| FT | DOMAIN | 1955 | 2068 | KRINGLE TYPE IV, 18. |
| FT | DOMAIN | 2069 | 2182 | KRINGLE TYPE IV, 19. |
| FT | DOMAIN | 2183 | 2296 | KRINGLE TYPE IV, 20. |
| FT | DOMAIN | 2297 | 2410 | KRINGLE TYPE IV, 21. |
| FT | DOMAIN | 2411 | 2524 | KRINGLE TYPE IV, 22. |
| FT | DOMAIN | 2525 | 2638 | KRINGLE TYPE IV, 23. |
| FT | DOMAIN | 2639 | 2752 | KRINGLE TYPE IV, 24. |
| FT | DOMAIN | 2753 | 2866 | KRINGLE TYPE IV, 25. |
| FT | DOMAIN | 2867 | 2980 | KRINGLE TYPE IV, 26. |
| FT | DOMAIN | 2981 | 3094 | KRINGLE TYPE IV, 27. |
| FT | DOMAIN | 3095 | 3208 | KRINGLE TYPE IV, 28. |
| FT | DOMAIN | 3209 | 3322 | KRINGLE TYPE IV, 29. |
| FT | DOMAIN | 3323 | 3436 | KRINGLE TYPE IV, 30. |
| FT | DOMAIN | 3437 | 3550 | KRINGLE TYPE IV, 31. |
| FT | DOMAIN | 3551 | 3664 | KRINGLE TYPE IV, 32. |
| FT | DOMAIN | 3665 | 3770 | KRINGLE TYPE IV, 33. |
| FT | DOMAIN | 3771 | 3884 | KRINGLE TYPE IV, 34. |
| FT | DOMAIN | 3885 | 3998 | KRINGLE TYPE IV, 35. |
| FT | DOMAIN | 3999 | 4112 | KRINGLE TYPE IV, 36. |
| FT | DOMAIN | 4113 | 4226 | KRINGLE TYPE IV, 37. |
| FT | DOMAIN | 4227 | 4327 | KRINGLE TYPE V. |
| FT | DOMAIN | 4328 | 4548 | SERINE PROTEASE. |
| FT | ACT_SITE | 4369 | 4369 | CHARGE RELAY SYSTEM. |
| FT | ACT_SITE | 4412 | 4412 | CHARGE RELAY SYSTEM. |
| FT | ACT_SITE | 4498 | 4498 | CHARGE RELAY SYSTEM. |
| FT | ACT_SITE | 4193 | 4193 | W -> R (LOSS OF LYSINE-SEPHAROSE BINDING). |
| FT | ACT_SITE | 4193 | 4193 | FTID=VAR 006633. |
| SO | SEQUENCE | 4548 AA; | 501313 MM; | 96921EB96A465C5F CRC64; |
| Query Match | Beat Local Similarity | 98.9%; | Score 517; | DB 1; Length 4548; |
| Matches | 88; Conservative | 0; | Pred. No. 4.1e-47; | Mismatches 1; Indels 0; Gaps 0; |
| QY | 1 | VRCYTHNGGOSYRGTSTTYTGRCQSSNSTPHRHQRTPEPNYNDGLTMNYCRNPADT | 60 | |
| DB | 4121 | VRCYTHNGGOSYRGTSTTYTGRCQSSNSTPHRHQRTPEPNYNDGLTMNYCRNPADT | 4180 | |
| QY | 61 | GPWCFTDPDSIRWEYCNLTRCSDEGTIV | 89 | |
| DB | 4181 | GPWCFTDPDSIRWEYCNLTRCSDEGTIV | 4209 | |
| RESULT 2 | | | | |
| ID | AP0A_MACMU | STANDARD; | PRT: | 1420 AA. |
| AC | P14417; | | | |
| DT | 01-JAN-1990 | (Rel. 13, Created) | | |
| DT | 01-JAN-1990 | (Rel. 13, Last sequence update) | | |
| DT | 28-FEB-2003 | (Rel. 41, Last annotation update) | | |
| DE | Apolipoprotein(a) (EC 3.4.21.-) (Apo(a)) (Lp(a)) (Fragment). | | | |
| GN | LpA. | | | |
| OS | Macaca mulatta (Rhesus macaque). | | | |
| OC | Eukaryota; Metazoa; Chordata; Ciniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; | | | |
| OC | Cercopitheidae; Macaca. | | | |
| OX | NCBI_TaxID=9544; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=89174660; PubMed=2925643; | | | |
| RA | Tomlinson J.E., McLean J.W., Lawn R.M.; | | | |
| RT | "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis." | | | |

CC J. Biol. Chem. 264:5957-5965(1989).
CC -1- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
CC (Lp(a)). It has serine proteinase activity and is able of
CC autoproteolysis. Inhibits tissue-type plasminogen activator 1.
CC Lp(a) may be a ligand for megalin/Gp 330.
CC -1- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
CC decorin (By similarity).
CC -1- PTM: N- and O-glycosylated (By similarity).
CC -1- DISEASE: Elevated plasma concentrations of apo(a) and its
CC naturally occurring proteolytic fragments are correlated with
CC atherosclerosis. Homology with plasminogen kringle IV and V is
CC thought to underlie the atherogenicity of the protein, because the
CC fragments are competing with plasminogen for fibrin(ogen) binding.
CC MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
CC leading to the formation of the so called mini-Lp(a). Apo(a)
CC fragments accumulate in atherosclerotic lesions, where they may
CC promote thromogenesis. O-glycosylation may limit the extent of
CC proteolytic fragmentation (By similarity).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains at least 10 kringle domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL, J04635; AAA36833.1; -
CC PIR, A32869; A32869.
CC HSP, P00747; 2PKA.
CC MEROPS: S01.226; -
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR001254; Ser_protease_Try.
CC Pfam: PF00051; kringle; 11.
CC Pfam: PF00089; trypsin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00018; KRINGLE.
CC ProDom: PD000395; Kringle; 10.
CC SMART: SM00130; KR; 10.
CC SMART: SM00020; Tryp_Spc; 1.
CC PROSITE: PS00021; KRINGLE_1; 10.
CC PROSITE: PS00070; KRINGLE_2; 10.
CC PROSITE: PS00240; TRYPSIN_DOM; 1.
CC PROSITE: PS00134; TRYPSIN_HIS; FALSE NEG.
CC PROSITE: PS00135; TRYPSIN_SER; FALSE NEG.
CC HydroLase: Serine proteinase; Lipid transport; Plasma; Glycoprotein;
KW Kringle; Repeat; Atherosclerosis.
KW NON_TER
FT DOMAIN 1 127 KRINGLE 1.
FT DOMAIN 163 241 KRINGLE 2.
FT DOMAIN 277 355 KRINGLE 3.
FT DOMAIN 391 469 KRINGLE 4.
FT DOMAIN 505 583 KRINGLE 5.
FT DOMAIN 619 697 KRINGLE 6.
FT DOMAIN 725 803 KRINGLE 7.
FT DOMAIN 839 917 KRINGLE 8.
FT DOMAIN 953 1031 KRINGLE 9.
FT DOMAIN 1067 1145 KRINGLE 10.
FT DOMAIN 1191 1420 SERINE PROTEASE.
SQ SEQUENCE 1420 AA; 158367 MW; BE102949E03C5B0E CRC64;

Query Match 91.4%; Score 478; DB 1; Length 1420;
Best Local Similarity 91.0%; Pred. No. 1.8e-43;
Matches 81; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

1 VVOCHGNGSQYRGFTSTVTGRTCSNNSMTPHQRQRTPEYVNDGLTMATCRPPDADT 60
1065 VVOCHGNGSQYRGFTSTVTGRTCSNNSMTPHQRQRTPEYVNDGLTMATCRPPDADT 1124
61 GPCFTTDPISRWYECNLTFRCSDEGTIV 89

DB 1125 GPCFTTDPISRWYECNLTFRCSDEGTIV 1153
|||||
RESULT 3
ID PLNN_HUMAN STANDARD; PRT; 810 AA.
AC P00747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Plasminogen precursor (BC 3.4.21.7) [Contains: Angiostatin].
GN Plg.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=90202879; PubMed=2318848;
RA Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;
RT "Characterization of the gene for human plasminogen, a key proenzyme
RT in the fibrinolytic system.";
RL J. Biol. Chem. 265:6104-6111(1990).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=87162490; PubMed=3030813;
RA Forgren M., Raden B., Israelsen M., Larsson K., Heden L.-O.;
RT "Molecular cloning and characterization of a full-length cDNA clone
RT for human plasminogen.";
RL FEBS Lett. 213:254-260(1987).
RN (3)
RP SEQUENCE OF 20-810.
RA Sottrup-Jensen L., Petersen T.E., Magnusson S.;
RL Submitted (JUL-1977) to the PIR data bank.
RN (4)
RP SEQUENCE OF 292-810 FROM N.A.
RX MEDLINE=85023311; PubMed=6148961;
RA Malinowski D.P., Sadler J.E., Davie E.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT human and bovine plasminogen.";
RL Biochemistry 23:4243-4250(1984).
RN (5)
RP SEQUENCE OF 20-100.
RX MEDLINE=75093329; PubMed=122932;
RA Wiman B., Wallen P.;
RT "Structural relationship between 'glutamic acid' and 'lysine' forms
RT of human plasminogen and their interaction with the NH2-terminal
RT activation peptide as studied by affinity chromatography.";
RL Eur. J. Biochem. 50:489-494(1975).
RN (6)
RP SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810.
RA Sottrup-Jensen L., Claess H., Zajdel M., Petersen T.E., Magnusson S.;
RL (in) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);
RT Progress in chemical fibrinolysis and thrombolysis, pp.3.191-209,
RL Raven Press, New York (1978).
RN (7)
RP SEQUENCE OF 483-604.
RX MEDLINE=76043692; PubMed=126863;
RA Wiman B., Wallen P.;
RT "Amino-acid sequence of the cyanogen-bromide fragment from human
RT plasminogen that forms the linkage between the plasmin chains.";
RL Eur. J. Biochem. 58:539-547(1975).
RN (8)
RP SEQUENCE OF 581-810.
RX MEDLINE=77225245; PubMed=142009;
RA Wiman B.;
RT "Primary structure of the B-chain of human plasmin.";
RL Eur. J. Biochem. 76:129-137(1977).
RN (9)
RP ACTIVE SITE.
RX MEDLINE=73149248; PubMed=4694729;
RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;

RT "The primary structure of human plasminogen-II. The histidine loop
RT of human plasmin: light (B) chain active center histidine sequence." ;
RL J. Biol. Chem. 248:1631-1633 (1973).
RN (10)
RP ACTIVE SITE.
RX MEDLINE=69234739; PubMed=4420117;
RA Grosofopf W.R., Summaria L., Robbins K.C.;
RT "Studies on the active center of human plasmin. Partial amino acid
RT sequence of a peptide containing the active center serine residue."
RL J. Biol. Chem. 244:3590-3597 (1969).
RN (11)
RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RX MEDLINE=82213905; PubMed=6919539;
RA Tixeler M., Vail Z., Patchy L.;
RT "Structure of the omega-aminocarboxylic acid-binding sites of human
RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
RT binding of ligand by kringle 4." ;
RL J. Biol. Chem. 257:7401-7406 (1982).
RN (12)
RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RX MEDLINE=85054794; PubMed=6094526;
RA Vail Z., Patchy L.;
RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
RT are essential for fibrin affinity of the kringle 1 domain." ;
RL J. Biol. Chem. 259:113690-113694 (1984).
RN (13)
RP PHOSPHORYLATION SITE SER-597.
RX MEDLINE=97345939; PubMed=9201958;
RA Wang H., Proctor M., Bretthauer R.K., Castellino F.J.;
RT "Serine-578 is a major phosphorylation locus in human plasma
RT plasminogen." ;
RL Biochemistry 36:8100-8106 (1997).
RN (14)
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185329; PubMed=3356193;
RA Meriti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns." ;
RL Eur. J. Biochem. 173:57-63 (1988).
RN (15)
RP CARBOHYDRATE-LINKAGE SITE SER-268.
RX MEDLINE=97207306; PubMed=9054441;
RA Plite-Shopheard S.R., Stevens R.D., Andon N.L., Enghild J.J.,
RA Pizzo S.V.;
RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
RT human plasminogen 2." ;
RL J. Biol. Chem. 272:7408-7411 (1997).
RN (16)
RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX MEDLINE=95042728; PubMed=7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA Moses M., Iane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma." ;
RL Cell 79:315-328 (1994).
RN (17)
RP CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE=97238710; PubMed=9102221;
RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Maden J.W.,
RA Lapcevic R., Nacy C.A.;
RT "A recombinant human angiostatin protein inhibits experimental primary
RT and metastatic cancer." ;
RL Cancer Res. 57:1329-1334 (1997).
RN (18)
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE=92031502; PubMed=16571149;
RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
RT "Crystal and molecular structure of human plasminogen kringle 4
RT refined at 1.9-A resolution." ;
RL Biochemistry 30:10576-10588 (1991).
RN (19)

RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE=92031503; Pubmed=1657149;
RA Wu T.-P., Padmanabhan K., Tulinaky A., Mullick A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of
RT human plasminogen kringle 4.";
RL Biochemistry 30:10589-10594(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RA Stec B., Yamano A., Whitlow M., Teeter M.M.;
RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.
RT A possible structural role of disordered residues.";
RL Acta Crystallogr. D 53:169-178(1997).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
RX MEDLINE=96180681; Pubmed=8611560;
RA Mathews I.I., Vanderhoff-Hanover P., Castellino F.J., Tulinaky A.;
RT "Crystal structures of the recombinant kringle 1 domain of human
RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic Acid.";
RL Biochemistry 35:2567-2576(1996).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
RX MEDLINE=96198034; Pubmed=9521645;
RA Chang Y., Mochalkin I., McCance S.G., Cheng B., Tulinaky A.,
RA Castellino F.J.;
RT "Structure and ligand binding determinants of the recombinant kringle
RT 5 domain of human plasminogen.";
RL Biochemistry 37:3258-3271(1998).
RN [23]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237157; Pubmed=8181475;
RA Rejzner M.R., Llinas M.;
RT "1H-NMR assignments and secondary structure of human plasminogen
RT kringle 1.";
RL Eur. J. Biochem. 221:927-937(1994).
RN [24]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237158; Pubmed=8181476;
RA Rejzner M.R., Llinas M.;
RT "Solution structure of the epsilon-aminohexanoic acid complex of
RT human plasminogen kringle 1.";
RL Eur. J. Biochem. 221:939-949(1994).
RN [25]
RP STRUCTURE BY NMR OF 183-354.
RX MEDLINE=96194156; Pubmed=8652577;
RA Soemmel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
RA Rickli B.G.;
RT "Recombinant gene expression and 1H NMR characteristics of the
RT kringle (2 + 3) supermodule: spectroscopic/functional individuality
RT of plasminogen kringle domains";
RL Biochemistry 35:2357-2364(1996).
RN [26]
RP STRUCTURE BY NMR OF 374-461.
RX MEDLINE=90219023; Pubmed=2157850;
RA Atkinson R.A., Williams R.J.P.;
RT "Solution structure of the kringle 4 domain from human plasminogen by
RT 1H nuclear magnetic resonance spectroscopy and distance geometry.";
RL J. Mol. Biol. 212:541-552(1990).
RN [27]
RP VARIANTS PHE-374 AND THR-620.

[illegible]

RESULT 4
PLAN MACMU
ID PLAN MACMU STANDARD; PRT; 810 AA.
AC P12545;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7).
GN PLG.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=89174660; PubMed=2925643;
RA Tomlinson J.E., McLean J.W., Lawn R.M.;
RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
synthesis";
RL J. Biol. Chem. 264:5957-5965(1989).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
higher selectivity than trypsin. Converts fibrin into soluble
products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STEPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN 2 CHAINS HELD
TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: contains 5 kringle domains.
CC -----
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CC -----
DR EMBL; J04697; AAA36901.1; -
DR PIR; B32869; B30848.
DR HSSP; P00747; 1PMK.
DR MEROPS; S01.233;
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; PAN_APP.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PS00021; KRINGLE 1; 5.
DR PROSITE; PS50070; KRINGLE 2; 5.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyse; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 810 PLASMINOGEN.
FT CHAIN 20 580 PLASMIN HEAVY CHAIN A.
FT PEPTIDE 20 96 ACTIVATION PEPTIDE.
FT CHAIN 97 580 PLASMIN SHORT FORM OF CHAIN A.
FT CHAIN 581 810 PLASMIN LIGHT CHAIN B.
FT CHAIN 103 181 KRINGLE 1.
FT DOMAIN 184 262 KRINGLE 2.
FT DOMAIN 275 352 KRINGLE 3.
FT DOMAIN 377 454 KRINGLE 4.
FT DOMAIN 481 560 KRINGLE 5.
FT DOMAIN 581 810 SERINE PROTEASE.
FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
FT ACT_SITE 655 655 CHARGE RELAY SYSTEM.
FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
FT BINDING 136 136 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 158 158 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 172 172 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 432 432 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 134 134 FIBRIN.
FT BINDING 136 136 FIBRIN.
FT DISULFID 49 73 BY SIMILARITY.
FT DISULFID 53 61 BY SIMILARITY.
FT DISULFID 103 181 BY SIMILARITY.
FT DISULFID 124 164 BY SIMILARITY.
FT DISULFID 152 176 BY SIMILARITY.
FT DISULFID 185 262 BY SIMILARITY.
FT DISULFID 188 316 BY SIMILARITY.
FT DISULFID 206 245 BY SIMILARITY.
FT DISULFID 234 257 BY SIMILARITY.
FT DISULFID 275 352 BY SIMILARITY.
FT DISULFID 326 335 BY SIMILARITY.
FT DISULFID 347 454 BY SIMILARITY.
FT DISULFID 377 437 BY SIMILARITY.
FT DISULFID 398 437 BY SIMILARITY.
FT DISULFID 426 449 BY SIMILARITY.
FT DISULFID 481 560 BY SIMILARITY.
FT DISULFID 502 543 BY SIMILARITY.
FT DISULFID 531 555 BY SIMILARITY.
FT DISULFID 567 685 BY SIMILARITY.
FT DISULFID 577 585 BY SIMILARITY.
FT DISULFID 607 623 BY SIMILARITY.
FT DISULFID 699 766 BY SIMILARITY.
FT DISULFID 729 745 BY SIMILARITY.
FT DISULFID 756 784 BY SIMILARITY.
FT CARBOHYD 365 365 O-LINKED (GLNAC...) (BY SIMILARITY).
SQ SEQUENCE 810 AA; 90255 MW; A75E1C51A0E224A CMC64;

Query Match 82.8%; Score 433; DB 1; Length 810;
Best Local Similarity 79.5%; Pred. No. 6.5e-39;
Matches 70; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 VROCHNGSGSYRGFTTGTGRTGOSWSMTPHRHQTPENYPRDGLTMNYCRNPADDT 60
DB 374 VQECTHGSGSYRGFTTGTGRTGOSWSMTPHRHQTPENYPRDGLTMNYCRNPADDT 433
QY 61 GPWCFTDPSIRWEXCNLTRCSDEGTGTV 88
DB 434 GPWCFTDPSIRWEXCNLTRCSDEGTGTV 461

RESULT 5
PLAN BOVIN
ID PLAN BOVIN STANDARD; PRT; 812 AA.

AC p06868: 028162;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7).
GN PLG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Berglund L., Andersen M.D., Petersen T.E.;
RT "Cloning and characterization of the bovine plasminogen cDNA.";
RL Int. Dairy J. 5:593-603(1995).
RN [2]
RX SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=65203906; Pubmed=3846532;
RA Schaller J., Moser P.W., Dammegeer-Mueller G.A.K., Rosselet S.J.,
RA Kampfer U., Rickli E.E.;
RT "Complete amino acid sequence of bovine plasminogen. Comparison with
RT human plasminogen.";
RL Eur. J. Biochem. 149:267-278(1985).
RN [3]
RP SEQUENCE OF 706-812 FROM N.A.
RP MEDLINE=65023311; Pubmed=6148961;
RA Malinowski D.P., Sadler J.E., Davie E.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT human and bovine plasminogen.";
RL Biochemistry 23:4243-4250(1984).
RN [4]
RP CARBOHYDRATE-LINKAGE SITES.
RP MEDLINE=68185329; Pubmed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamberling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION; IT ACTIVATES THE URKINASE-TYPE PLASMINOGEN
CC GAAPIAN FOLICLE. IT ACTIVATES THE URKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOSINS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STEPTOKINASE.
CC -1- PTM: N-LINKED GLYCAN CONTAIN N-ACETYLGLUCOSAMINE AND SIALIC ACID.
CC O-LINKED GLYCANS CONSIST OF GAL-GALNA6 DISACCHARIDE WITH IS
CC MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kringle domains.
CC -----
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CC or send an email to license@isb-sib.ch).
OR EMBL; X79402; CAA55939.1; -
OR EMBL; K02935; AAA30714.1; -
OR

[illegible]

RP Sus scrofa (Pig).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE OF 1-560.
 RA Schaller T., Marti T., Roeselele S.J., Kaempfer U., Rickli E.E.;
 RT "Amino acid sequence of the heavy chain of porcine plasmin. Comparison
 RT of the carbohydrate attachment sites with the human and bovine
 RT species";
 RL Fibrinolysis 1:91-102(1987).
 RN [2]
 RP SEQUENCE OF 450-790.
 RX MEDLINE=85203907; PubMed=3846533;
 RA Marti T., Schaller J., Rickli E.E.;
 RT "Determination of the complete amino-acid sequence of porcine
 RT miniplasminogen.";
 RL Eur. J. Biochem. 149:279-285(1985).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=8815329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
 RA Gewig G.J., van Halbeek H., Vliegenthart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to sialylation and
 RT fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRANULOSA FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PPM: N-LINKED GLYCAN CONTAINS N-ACETYLLACTOSAMINE, SALIC ACID AND
 CC IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAIC
 CC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
 CC (MICROHETEROGENEITY).
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 DR HSSP; P00747, SHPG.
 DR MEROPS; S01.233; -.
 DR Glycosylated; P06867; -.
 DR Interpro; IPR001314; Chymotrypsin.
 DR Interpro; IPR000001; Kringle.
 DR Interpro; IPR003014; PAN.
 DR Interpro; IPR003609; pan_app.
 DR Interpro; IPR003966; Prochombin.
 DR Interpro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00051; kring1; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kring1; 5.
 DR SMART; SM00473; PAN AP; 1.
 DR SMART; SM00473; PAN AP; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; FALSE NEG.

DR PROSITE; PS00135; TRYPSIN SER. 1.
KW Hydroxylase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
FT CHAIN 1
FT CHAIN 560
FT DOMAIN 561 790 PLASMIN HEAVY CHAIN A.
FT DOMAIN 561 790 SERINE PROTEASE.
FT DOMAIN 84 162 KRINGLE 1.
FT DOMAIN 166 243 KRINGLE 2.
FT DOMAIN 256 333 KRINGLE 3.
FT DOMAIN 358 435 KRINGLE 4.
FT DOMAIN 461 540 KRINGLE 5.
FT ACT_SITE 602 602 CHARGE RELAY SYSTEM.
FT ACT_SITE 645 645 CHARGE RELAY SYSTEM.
FT ACT_SITE 740 740 CHARGE RELAY SYSTEM.
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
FT CARBOHYD 340 340 /FTID=CAR.000019.
FT CARBOHYD 340 340 /FTID=CAR.000020.
SQ SEQUENCE 790 AA; 88592 MW; P04BA06E74BCD58B CMC64;
Query Match 76.7%; Score 401; DB 1; Length 790;
Best Local Similarity 73.6%; Pred. No. 1.7e-35;
Matches 64; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
OY 2 RQCHNGGSGYRGFFSTTVTCRTQSSMSMTPHRHQRPRXPYDGLTMVCRPPDADTG 61
DB 356 QDCRCRGESRGTSSTTIGTRKQSVSWMTPHRHKTPGNFPVNAGLTMVCRPPDADS 415
OY 62 PMCEETDPSIRMEYCNLTRECSDTEGTV 88
DB 416 PMCTTDPYRMEYCNLKCKSETTQGV 442
RESULT 7
PLAN_MOUSE STANDARD; PRT; 812 AA.
ID PLAN_MOUSE
AC P20918; Q8C1S2; Q91WU5.
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Plasmalogen precursor (EC 3.4.21.7) [Contains: Angiotatin].
GN PLG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91184812; PubMed=2081600;
RA Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
RT "Characterization of the cDNA coding for mouse plasmalogen and
RL localization of the gene to mouse chromosome 17.";
RL Genomics 8:49-61(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SV;
RA Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
RA Nagaraja R.;
RT "Genomic sequence analysis in the mouse t-complex region.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jorde H., Moore T., Max S.I., Wang J., Hsieh F.,
RA DiCicco L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywiński M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [4]
 RN SEQUENCE OF 1-16 FROM N.A.
 RC STRAIN=129/Svj; TISSUE=Liver;
 RX PubMed=12149246;
 RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
 RA Farmer R.J., Miles L.A.,
 RT "Localization of regulatory elements mediating constitutive and
 RT cytokine-stimulated plasminogen gene expression.";
 RL J. Biol. Chem. 277:38579-38588(2002).
 RN [5]
 RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
 RX MEDLINE=95042728; PubMed=7525077;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RA Moses M., Lane W.S., Cao Y., Sage B.H., Folkman J.,
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
 RT suppression of metastases by a Lewis lung carcinoma.";
 RL Cell 79:315-328(1994).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
 CC NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
 CC METASTATIC TUMORS IN VIVO.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
 CC INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD
 CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
 CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 5 kringle domains.
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 CC -----
 CC EMBL: J04766; AAA50168.1; -;
 CC EMBL: AF481053; AA022156.1; -;
 CC EMBL: BC014773; AA014773.1; -;
 CC EMBL: AY134430; AA015805.1; -;
 CC PIR: A38514; PLMS.
 CC HSSP: P00747; LPMK.
 CC MEROPS: S01.233; -;
 CC MCD; MGI:97620; P19.
 CC GO; GO:0016506; F:apoptosis activator activity; IDA.
 CC GO; GO:0006915; P:apoptosis; IDA.
 CC InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan. app.
 DR InterPro; IPR003966; Prochrombin.
 DR InterPro; IPR001254; Ser. protease_Try.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN AP; 1.
 DR SMART; SM00020; Tryp. Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00740; KRINGLE_2; 5.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 KM Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KM Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KW Signal.
 FT SIGNAL. 1 19
 FT CHAIN 20 812 PLASMINOGEN.
 FT CHAIN 20 581 PLASMIN HEAVY CHAIN A.
 FT PEPTIDE 20 97 ACTIVATION PEPTIDE.
 FT CHAIN 98 581 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 98 7436 ANGIOSTATIN.
 FT CHAIN 582 812 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 103 181 KRINGLE 1.
 FT DOMAIN 184 262 KRINGLE 2.
 FT DOMAIN 275 352 KRINGLE 3.
 FT DOMAIN 377 454 KRINGLE 4.
 FT DOMAIN 481 560 KRINGLE 5.
 FT 582 812 SERINE PROTEASE.
 FT ACT SITE 624 624 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT SITE 667 667 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 49 73 BY SIMILARITY.
 FT DISULFID 53 61 BY SIMILARITY.
 FT DISULFID 103 181 BY SIMILARITY.
 FT DISULFID 124 164 BY SIMILARITY.
 FT DISULFID 152 176 BY SIMILARITY.
 FT DISULFID 185 262 BY SIMILARITY.
 FT DISULFID 188 316 BY SIMILARITY.
 FT DISULFID 206 245 BY SIMILARITY.
 FT DISULFID 234 257 BY SIMILARITY.
 FT DISULFID 275 352 BY SIMILARITY.
 FT DISULFID 296 335 BY SIMILARITY.
 FT DISULFID 324 347 BY SIMILARITY.
 FT DISULFID 377 454 BY SIMILARITY.
 FT DISULFID 398 437 BY SIMILARITY.
 FT DISULFID 426 449 BY SIMILARITY.
 FT DISULFID 481 560 BY SIMILARITY.
 FT DISULFID 502 543 BY SIMILARITY.
 FT DISULFID 531 555 BY SIMILARITY.
 FT DISULFID 568 687 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 578 586 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 609 625 BY SIMILARITY.
 FT DISULFID 701 747 BY SIMILARITY.
 FT DISULFID 731 747 BY SIMILARITY.
 FT DISULFID 758 786 BY SIMILARITY.
 FT CONFLICT 235 235 R -> H (IN REF. 1).
 FT CONFLICT 525 525 G -> D (IN REF. 1).
 FT CONFLICT 649 649 S -> L (IN REF. 1).
 SQ SEQUENCE 812 AA; 90781 MW; 241732605A2FFD2 CRC64;

Query Match 76.5%; Score 400; DB 1; Length 812;
 Best Local Similarity 70.8%; Pred. No. 2,3e-35;
 Matches 63; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
 QY 1 VROCYHNGQSYKRGFTSTVLTGRTCSWSSMTPHRQRTPEPNYNDGLTMNTGRNPDADT 60


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Db 374 VQECYSDGSGYRGSTSTITTKGCKOSWAMFPHRSKTPENPDAGLEMYCRNPDGDK 433
Qy 61 GPMCFITDPSIRWEXCNLTRCSGTEHYV 89
Db 434 GPMCFITDPSIRWEXCNLTRCSGTEHYV 462

RESULT 8
PLMN_ERIEU STANDARD; PRT; 810 AA.
AC Q29485;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7).
GN PLG.
OS Etrineus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96025778; PubMed=7592597;
RA Byrne C.D., Fong K.J., Meer K., Patchy L.,
RA Lawn R.M., Boomark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
RT "The recurring evolution of lipoprotein(a). Insights from cloning of
RT hedgehog apolipoprotein(a).".
RT J. Biol. Chem. 270:24004-24009(1995).
RN [2]
RP REVISIONS.
RA Lawn R.M.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION. IT WEAKENS THE WALLS OF THE
CC GRAFIAN FOLLICLE. IT ACTIVATES THE UKOKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kringle domains.
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL, U31171; AAC48717.1; -.
CC DR PIR, I46260; I46260.
CC DR HSSP, P00747; IPMK.
CC DR MEROPS, S01.233; -.
CC DR InterPro: IPR001314; Chymotrypsin.
CC DR InterPro: IPR003001; Kringle.
CC DR InterPro: IPR003014; PAN.
CC DR InterPro: IPR003609; Pan_app.
CC DR InterPro: IPR003966; Prothrombin.
CC DR InterPro: IPR001254; Ser_protease_Try.
CC DR Pfam, PF00051; kringle_5.
CC DR Pfam, PF00024; PAN; 1.

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DR Pfam, PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00020; KRINGLE_1; 5.
DR PROSITE; PS00020; KRINGLE_2; 5.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Hydrolase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KM Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KW Signal.
FT SIGNAL. 1 19 BY SIMILARITY.
FT CHAIN 20 810 PLASMINOGEN.
FT CHAIN 20 582 PLASMIN HEAVY CHAIN A (BY SIMILARITY).
FT CHAIN 583 810 PLASMIN LIGHT CHAIN B (BY SIMILARITY).
FT DOMAIN 583 810 SERINE PROTEASE.
FT DOMAIN 103 181 KRINGLE 1.
FT DOMAIN 185 262 KRINGLE 2.
FT DOMAIN 379 456 KRINGLE 3.
FT DOMAIN 479 561 KRINGLE 4.
FT DOMAIN 482 622 KRINGLE 5.
FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
FT CARBOHYD 339 339 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 810 AA; 90902 MW; 8E7578046017A16 CRC64;

Query Match 75.0%; Score 192; DB 1; Length 810;
Best Local Similarity 71.8%; Pred.No.1.6e-34;
Matches 61; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VROCCHNGGSGYRGSTSTITTKGCKOSWMTPHRQTPENPDAGLEMYCRNPDGDT 60
Db 376 VQECYSDGSGYRGSTSTITTKGCKQPTSMRPHRSKTPENPDAGLEMYCRNPDGDK 435
Qy 61 GPMCFITDPSIRWEXCNLTRCSGTE 85
Db 436 GPMCFITDPSIRWEXCNLTRCSGTE 460

RESULT 9
PLMN_RAT STANDARD; PRT; 169 AA.
AC Q00177;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN PLG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91250378; PubMed=1645711;
RA Kanalas J.J., Makker S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
RT receptor site for plasminogen."
RT J. Biol. Chem. 266:10825-10829(1991).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION. IT ACTIVATES THE UKOKINASE-TYPE PLASMINOGEN
CC GRAFIAN FOLLICLE. IT ACTIVATES THE UKOKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,

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CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kringle domains.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M62832; AAA41884.1; -.
CC PIR: A40522; A40522.
CC HSSP: P00747; 1PMK.
CC MEROPS: S01.233; -.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR003966; Prothrombin.
CC InterPro: IPR001254; Ser. protease_Try.
CC Pfam: PF00051; Kringle; 2.
CC PRINTS: PR00018; KRINGLE.
CC PRINTS: PR01505; PROTHROMBIN.
CC ProDom: PD000395; Kringle; 2.
CC SMART: SM00130; KR; 1.
CC PROSITE: PS00021; KRINGLE 1; 1.
CC PROSITE: PS50070; KRINGLE 2; 2.
CC PROSITE: PS50240; TRYPSIN_DOM; PARTIAL.
CC PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
CC PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
CC Hydrolase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
CC Tissue remodeling; Blood coagulation; Kringle; Repeat.
CC -----
CC NON_TER 1
CC DOMAIN <1 10 KRINGLE 3 (BY SIMILARITY).
CC DOMAIN 34 112 KRINGLE 4 (BY SIMILARITY).
CC DOMAIN 139 >169 KRINGLE 5 (BY SIMILARITY).
CC DISULFID 34 112 BY SIMILARITY.
CC DISULFID 55 95 BY SIMILARITY.
CC DISULFID 83 107 BY SIMILARITY.
CC NON_TER 169 169
CC SEQUENCE 169 AA; 18401 MW; 77A54214C49D010C CRC64;
Query Match 72.9%; Score 381.5; DB 1; Length 169;
Best Local Similarity 71.9%; Pred. No. 3.9e-34;
Matches 64; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
Qy 1 VROCYHNGSGSYRGTFTYTGRTQSWSMTPRHQRTPENYPNDLTMYNCMPAD- 59
Db 31 VQECYQNGSGSYRGTFTYTGRTQSWSMTPRHQRTPENYPNDLTMYNCMPAD- 90
Qy 60 TGPWCFTTDPSSIRWEYCNLTRCSTBETV 88
Db 91 RGPWCFTTDPSSIRWEYCNLTRCSTBETV 119
RESULT 10
HGFL_MOUSE STANDARD; PRT; 716 AA.
ID HGFL_MOUSE
AC P26928;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
DE stimulatory protein) (MSP).
GN MST1 OR HGFL.
OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID:10090;
CC RN
CC RP
CC SEQUENCE FROM N.A.
CC STRAIN=BALB/c; TISSUE=Liver;
CC MEDLINE:92002017; PubMed:1832957;
CC Fliener Degen S.J., Stuart L.A., Han S., Jamison C.S.;
CC "Characterization of the mouse cdna and gene coding for a hepatocyte
CC growth factor-like protein: expression during development.";
CC Biochemistry 30:9781-9791(1991).
CC RL
CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
CC CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
CC CONSERVED.
CC -1- TISSUE SPECIFICITY: LIVER. LOWER LEVELS IN LUNG, PLACENTA AND
CC ADRENAL.
CC -1- DEVELOPMENTAL STAGE: IS EXPRESSED AT LOW LEVELS DURING GESTATION.
CC JUST BEFORE BIRTH THE LEVEL INCREASES DRAMATICALLY AND REMAINS
CC STABLE AFTERWARDS.
CC -1- PTM: MAY BE CLEAVED AFTER AA 488, TO YIELD A TWO-CHAIN MOLECULE
CC HELD TOGETHER BY DISULFIDE BONDS, OR CLEAVED INTO TWO SEPARATE
CC POLYPEPTIDES
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 4 kringle domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M74180; AAA50166.1; -.
CC EMBL: M74181; AAA50167.1; -.
CC PIR: A40332; A40332.
CC HSSP: P00747; 1KRN.
CC MEROPS: S01.975; -.
CC MGD: MG1:96080; Mgt1.
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR003014; PAN.
CC InterPro: IPR003609; Pan_app.
CC InterPro: IPR003966; Prothrombin.
CC InterPro: IPR001254; Ser. protease_Try.
CC Pfam: PF00051; kringle; 4.
CC Pfam: PF00024; PAN; 1.
CC Pfam: PF00089; trypsin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00018; KRINGLE.
CC PRINTS: PR01505; PROTHROMBIN.
CC ProDom: PD000395; Kringle; 4.
CC SMART: SM00130; KR; 4.
CC SMART: SM00473; PAN_AP; 1.
CC SMART: SM00020; TRYD_SPC; 1.
CC PROSITE: PS00021; KRINGLE 1; 4.
CC PROSITE: PS50070; KRINGLE 2; 4.
CC PROSITE: PS50240; TRYPSIN_DOM; 1.
CC KRingle; Glycoprotein; Serine protease homolog; Repeat; Signal.
CC KW
CC STGNL 1 18
CC CHAIN 19 716
CC FT 19 109
CC FT DOMAIN 110 166
CC FT DOMAIN 191 268
CC FT DOMAIN 292 370
CC FT DOMAIN 379 457
CC FT DOMAIN 489 716
CC DISULFID 56 78
CC DISULFID 60 66
CC DISULFID 110 186
CC DISULFID 131 169
CC DISULFID 157 181
CC DISULFID 191 268
CC PAV.
CC HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.
CC KRINGLE 1.
CC KRINGLE 2.
CC KRINGLE 3.
CC KRINGLE 4.
CC SERINE PROTEASE-LIKE.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.

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FT DISULFID 194 333 INTERCHAIN (BY SIMILARITY).
FT DISULFID 212 251 BY SIMILARITY.
FT DISULFID 240 263 BY SIMILARITY.
FT DISULFID 292 370 BY SIMILARITY.
FT DISULFID 313 352 BY SIMILARITY.
FT DISULFID 341 364 BY SIMILARITY.
FT DISULFID 379 457 BY SIMILARITY.
FT DISULFID 400 440 BY SIMILARITY.
FT DISULFID 428 452 BY SIMILARITY.
FT DISULFID 477 593 INTERCHAIN (BY SIMILARITY).
FT DISULFID 512 528 BY SIMILARITY.
FT DISULFID 607 672 BY SIMILARITY.
FT DISULFID 637 651 BY SIMILARITY.
FT DISULFID 662 690 BY SIMILARITY.
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 19 19 P -> Q (IN GENOMIC SEQUENCE).
SQ SEQUENCE 716 AA; 80586 MW; B8CE02EF85213A0C CRC64;

Query Match 52.1%; Score 272.5; DB 1; Length 716;
Best Local Similarity 55.4%; Pred. No. 9.6e-22;
Matches 46; Conservative 11; Mismatches 25; Indels 1; Gaps 1;

QY 4 CHGNGSAGTSTVTGRTCSWSMPEHRORTPENPNGLMNYCRNPADT-GP 62
Db 379 CHGSGEQKRGVSQKTRKGVQCCWSETPHKQFPTPSAPQAGLEANFCRNDGSDHP 438
QY 63 WCPTTDSIRMEYCNLTRCSDE 85
Db 439 WCYTLDPDLFDYCALQRCDDQ 461

RESULT 11
HGF HUMAN STANDARD; PRT; 728 AA.
ID _HGF_HUMAN
AC P14210; O9BYL9; Q9UDU6;
DT 01-JUN-1990 (Rel. 13, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hepatocyte growth factor precursor (Scatter factor) (SF)
DE (Hepatopoietin A).
GN HGF OR HPTA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91340155; PubMed=1831432;
RA Seki T., Hagiya M., Shimomishi M., Nakamura T., Shimizu S.;
RT "Organization of the human hepatocyte growth factor-encoding gene.";
RL Gene 102:213-219 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=893392017; PubMed=2528952;
RA Miyazawa K., Teubouchi H., Naka D., Takahashi K., Okigaki M.,
RA Arakaki N., Nakayama H., Hiroo S., Sakiyama O., Takahashi K.,
RA Gohda E., Daikuhara Y., Kitamura N.;
RT "Molecular cloning and sequence analysis of cDNA for human hepatocyte
RT growth factor.";
RL Biochem. Biophys. Res. Commun. 163:967-973 (1989).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=91025062; PubMed=2145836;
RA Seki T., Ihara I., Sugimura A., Shimomishi M., Nishizawa T.,
RA Asami O., Hagiya M., Nakamura T., Shimizu S.;
RT "Isolation and expression of cDNA for different forms of hepatocyte
RT growth factor from human leukocyte.";
RL Biochem. Biophys. Res. Commun. 172:321-327 (1990).

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RN [4]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 55-73 AND 495-520.
RC TISSUE=Liver;
RX MEDLINE=9006676; PubMed=2531289;
RA Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimomishi M.,
RA Sugimura A., Tashiro K., Shimizu S.;
RT "Molecular cloning and expression of human hepatocyte growth factor.";
RL Nature 342:440-443 (1989).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic fibroblast;
RX MEDLINE=9134393; PubMed=1831266;
RA Weidner K.M., Arakaki N., Hartmann G., Vandeckerckhove J., Weingart S.,
RA Rieder H., Fontatsch C., Teubouchi H., Hishida T., Daikuhara Y.,
RA Birnmeier W.;
RT "Evidence for the identity of human scatter factor and human
RT hepatocyte growth factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005 (1991).
RN [6]
RP SEQUENCE FROM N.A.
RA Courtney L., Elliot G., Angell S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 249-695 FROM N.A.
RX MEDLINE=91369928; PubMed=1832556;
RA Miyazawa K., Kitamura A., Kitamura N.;
RT "Structural organization and the transcription initiation site of the
RT human hepatocyte growth factor gene.";
RL Biochemistry 30:9170-9176 (1991).
RN [8]
RP SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE=91207365; PubMed=1826837;
RA Yoshiyama Y., Arakaki N., Naka D., Takahashi K., Hiroo S., Kondo J.,
RA Nakayama H., Gohda E., Kitamura N., Teubouchi H., Ishii T.,
RA Hishida T., Daikuhara Y.;
RT "Identification of the N-terminal residue of the heavy chain of both
RT native and recombinant human hepatocyte growth factor.";
RL Biochem. Biophys. Res. Commun. 175:660-667 (1991).
RN [9]
RP CARBOHYDRATE-LINKAGE SITE THR-476.
RX MEDLINE=93129192; PubMed=1482348;
RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
RA Nakamura T., Shimizu S.;
RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
RT on the alpha chain.";
RL Biochem. Biophys. Res. Commun. 189:1329-1335 (1992).
RN [10]
RP MUTAGENESIS.
RX MEDLINE=92331602; PubMed=1321034;
RA Lokter N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
RA Baker J.B., Godowski P.J.;
RT "Structure-function analysis of hepatocyte growth factor:
RT identification of variants that lack mitogenic activity yet retain
RT high affinity receptor binding.";
RL EMBO J. 11:2503-2510 (1992).
RN [11]
RP STRUCTURE BY NMR OF 31-127.
RX MEDLINE=98154323; PubMed=9493272;
RA Zhou H., Mazulla M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,
RA Rubin J.S., Bottaro D.P., Byrd R.A.;
RT "The solution structure of the N-terminal domain of hepatocyte growth
RT factor reveals a potential heparin-binding site.";
RL Structure 6:109-116 (1998).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.
RX MEDLINE=99036858; PubMed=9817840;
RA Ulicsak M., Lokter N.A., Godowski P.J., de Vos A.M.;
RT "Crystal structure of the NK1 fragment of human hepatocyte growth
RT factor at 2.0-A resolution.";
RL Structure 6:1383-1393 (1998).
CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR NATURE PARENCHYMAL
CC HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND ACTS
CC AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.

```

IT HAS NO DETECTABLE PROTEASE ACTIVITY.
 -1- SUBUNIT. DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
 DISULFIDE BOND.
 -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 -1- SIMILARITY: Contains 4 Kringle domain.
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 DR EMBL; D90334; BAA1348.1; -;
 DR EMBL; D90318; BAA1348.1; JOINED.
 DR EMBL; D90319; BAA1348.1; JOINED.
 DR EMBL; D90320; BAA1348.1; JOINED.
 DR EMBL; D90322; BAA1348.1; JOINED.
 DR EMBL; D90323; BAA1348.1; JOINED.
 DR EMBL; D90324; BAA1348.1; JOINED.
 DR EMBL; D90325; BAA1348.1; JOINED.
 DR EMBL; D90326; BAA1348.1; JOINED.
 DR EMBL; D90327; BAA1348.1; JOINED.
 DR EMBL; D90328; BAA1348.1; JOINED.
 DR EMBL; D90329; BAA1348.1; JOINED.
 DR EMBL; D90330; BAA1348.1; JOINED.
 DR EMBL; D90331; BAA1348.1; JOINED.
 DR EMBL; D90332; BAA1348.1; JOINED.
 DR EMBL; D90333; BAA1348.1; JOINED.
 DR EMBL; M29145; AAA52650.1; -;
 DR EMBL; M60718; AAA52650.1; -;
 DR EMBL; X16323; CAA34387.1; -;
 DR EMBL; M73239; AAA64239.1; -;
 DR EMBL; M73240; AAA64297.1; -;
 DR EMBL; AC004960; AAC71655.1; -;
 DR EMBL; M75983; AAG53460.1; -;
 DR EMBL; M75972; AAG53460.1; JOINED.
 DR EMBL; M75973; AAG53460.1; JOINED.
 DR EMBL; M75974; AAG53460.1; JOINED.
 DR EMBL; M75975; AAG53460.1; JOINED.
 DR EMBL; M75976; AAG53460.1; JOINED.
 DR EMBL; M75977; AAG53460.1; JOINED.
 DR EMBL; M75978; AAG53460.1; JOINED.
 DR EMBL; M75979; AAG53460.1; JOINED.
 DR EMBL; M75980; AAG53460.1; JOINED.
 DR EMBL; M75981; AAG53460.1; JOINED.
 DR EMBL; M75982; AAG53460.1; JOINED.
 DR PIR; JH0579; JH0579.
 DR PDB; 2HGF; 24-JUN-98.
 DR PDB; 1BHT; 18-NOV-98.
 DR PDB; 1NK1; 29-DEC-99.
 DR MEROPS; S01.976; -;
 DR GlycoSuiteDB; P14210; -;
 DR Genew; HGNC:4893; HGF.
 DR MIM; 142409; -;
 DR GO; GO:0008083; F: growth factor activity; NAS.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00051; Kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0018; KRINGLE.
 DR Prodom; PD000395; Kringle; 4.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN; AP; 1.
 DR SMART; SM00020; TRYF_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.

DR PROSITE; PS00070; KRINGLE_2; 4.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 KW Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
 KW Signal; 3D-structure; Polymorphism; Pyroglutamate carboxylic acid.
 FT SIGNAL 1 31
 FT CHAIN 32 434
 FT CHAIN 495 728
 FT MOD_RES 32 32
 FT DOMAIN 32 127
 FT DOMAIN 128 206
 FT DOMAIN 211 288
 FT DOMAIN 305 383
 FT DOMAIN 391 469
 FT DOMAIN 495 728
 FT DISULFID 70 96
 FT DISULFID 74 84
 FT DISULFID 128 206
 Query Match 51.4%; Score 269; DB 1; Length 728;
 Best Local Similarity 51.9%; Pred. No. 2.3e-21;
 Matches 42; Conservative 9; Mismatches 30; Indels 0; Gaps 0;
 QY 3 QCTHNGGSGYRGFTSTYVGRGCGSSMTPRHQRTPEYNDGLTMYCRNPADTGP 62
 DB 210 ECWTCGSGSYRGIMDTSGKTCQKWDHOTPRHFKFLPRYPDKGDDNYCRNPQGP 269
 QY 63 WCFTTDPSTIRMEYCNLTRCS 83
 DB 270 WCYTLDPHTRMEYCAIKTCAD 290
 RESULT 12
 HGF_MOUSE STANDARD; PRT; 728 AA.
 ID HGF_MOUSE
 AC Q08648; O61662; O64007;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hepatocyte growth factor precursor (Scatter factor) (SF)
 DE (Hepatopoietin A).
 GN HGF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOPFORMS LONG AND SHORT), AND SEQUENCE OF 496-504.
 RC TISSUE=Mammary fibroblast;
 RX MEDLINE=94183257; PubMed=8135822;
 RA Sasaki M., Nishio M., Sasaki T., Enami J.;
 RT "Identification of mouse mammary fibroblast-derived mammary growth
 RT factor as hepatocyte growth factor";
 RL Biochem. Biophys. Res. Commun. 199; 772-779 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94363381; PubMed=8081873;
 RA Lee C.C., Kozak G.A., Yamada K.M.;
 RT "Structure, genetic mapping, and expression of the mouse Hgf/scatter
 RT factor gene";
 RL Cell Adhes. Commun. 1:101-111 (1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94060105; PubMed=8241272;
 RA Liu Y., Michalopoulos G.K., Zarnegar R.;
 RT "Molecular cloning and characterization of cDNA encoding mouse
 RT hepatocyte growth factor";
 RL Biochim. Biophys. Acta 1216:299-303 (1993).
 CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 CC HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND ACTS AS
 CC GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES. IT
 CC HAS NO DETECTABLE PROTEASE ACTIVITY.

```

CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
CC DISULFIDE BOND.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q08048-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q08048-2; Sequence=VSP_005408;
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 4 kringle domains.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; D10213; BAA01064.1; -
CC EMBL; D10213; BAA01065.1; -
CC EMBL; S71816; AAB31855.1; -
CC EMBL; X72307; CAA51054.1; ALT_INIT.
CC PIR; JC2117; A60185.
CC HSSP; P14210; 1BHT.
CC MEROPS; S01.982; -
CC MGD; MGI.96079; Hgf.
CC InterPro; IPR001314; Chymotrypsin.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR003014; PAN.
CC InterPro; IPR003609; Pan app.
CC InterPro; IPR001254; Ser_protease_Try.
CC Pfam; PF00051; kringle; 4.
CC Pfam; PF00024; PAN; 1.
CC Pfam; PF00089; clypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000395; Kringle; 4.
CC SMART; SM00130; KR; 4.
CC SMART; SM00473; PAN_Ap; 1.
CC SMART; SM00020; TRYD_Spc; 1.
CC PROSITE; PS00021; KRINGLE_1; 4.
CC PROSITE; PS00070; KRINGLE_2; 4.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
CC Signal; Alternative splicing; Epyrrolidone carboxylic acid.
CC SIGNAL; 1
CC CHAIN 33 495
CC CHAIN 496 728
CC MOD_RES 33 33
-----
CC DOMAIN 33 128
CC DOMAIN 129 207
CC DOMAIN 212 289
CC DOMAIN 306 384
CC DOMAIN 392 470
CC DOMAIN 496 728
CC DISULFID 71 97
CC DISULFID 75 85
CC DISULFID 488 607
CC CARBOHYD 295 295
CC CARBOHYD 403 403
CC CARBOHYD 563 563
CC CARBOHYD 656 656
CC VARSPLIC 163 167
-----
CC CONFLICT 344 344
CC CONFLICT 479 479
CC CONFLICT 564 564
CC SEQUENCE 728 AA; 82944 MM; A0381FC497534328 CRC64;
-----
Query Match 50.3%; Score 263; DB 1; Length 728;
Best Local Similarity 51.2%; Pred. No. 1e-20;

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Matches 41; Conservative 9; Mismatches 30; Indels 0; Gaps 0;
QY 3 OCYHNGGOSYRGTFSTVTRTCOSMSWTPIRHORTENTYNDLTMNCGNPADGCP 62
DB 211 ECMTGNSYRGPMHTSGKTCRWDOCTPHRHFLEPRIFDKGFDNNYCNPDGKRRP 270
QY 63 WCFTDPSIRMEYCNITRCS 82
DB 271 WCYTLDPDPTMEYCAIKTCA 290
-----
RESULT 13
HGF RAT
ID HGF RAT STANDARD; PRT; 728 AA.
AC P17945;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hepatocyte growth factor precursor (Scatter factor) (SF)
DE (Hepatopoietin A).
GN HGF
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Miscar; TISSUE=Liver;
RX MEDLINE=90222197; PubMed=2139229;
RA Toshito K., Hagiya M., Nishizawa T., Seki T., Shimonihi M.,
RA Shimizu S., Nakamura T.;
RT "Deduced primary structure of rat hepatocyte growth factor and
RT expression of the mRNA in rat tissues."
RL Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar; TISSUE=Liver;
RX MEDLINE=91031482; PubMed=2146117;
RA Okajima A., Miyazawa K., Kitamura N.;
RT "Primary structure of rat hepatocyte growth factor and induction of
RT its mRNA during liver regeneration following hepatic injury."
RL Eur. J. Biochem. 193:375-381(1990).
CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
CC HEPATOCYTE CELLS. SEEMS TO BE AN HEPATOTROPIC FACTOR, AND ACTS
CC AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
CC IT HAS NO DETECTABLE PROTEASE ACTIVITY.
CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
CC DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 4 kringle domains.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; D90102; BAA14133.1; -
CC EMBL; X54400; CAA38266.1; -
CC PIR; A35644; A35644.
CC HSSP; P14210; 1BHT.
CC MEROPS; S01.978; -
CC InterPro; IPR001314; Chymotrypsin.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR003014; PAN.
CC InterPro; IPR003609; Pan app.
CC InterPro; IPR001254; Ser_protease_Try.
CC Pfam; PF00051; kringle; 4.
CC Pfam; PF00024; PAN; 1.
CC Pfam; PF00089; clypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.

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DR PRINTS; PRO0018; KRINGLE.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS50070; KRINGLE_2; 4.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
KW Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
Signal; Fyrroldone carboxylic acid.
FT SIGNAL 1 32
FT CHAIN 33 495
FT CHAIN 496 728
FT MOD_RES 33 33
FT DOMAIN 33 128
FT DOMAIN 129 207
FT DOMAIN 212 289
FT DOMAIN 306 384
FT DOMAIN 392 470
FT DOMAIN 496 728
FT DISULFID 71 97
FT DISULFID 75 85
FT DISULFID 488 607
FT CARBOHYD 295 295
FT CARBOHYD 403 403
FT CARBOHYD 569 569
FT CARBOHYD 656 656
SQ SEQUENCE 728 AA; 82905 MW; 3E0BF1F96ADEDF CRC64;

Query Match 50.3%; Score 263; DB 1; Length 728;
Best Local Similarity 51.2%; Pred. No. 1e-20;
Matches 41; Conservative 9; Mismatches 30; Indels 0; Gaps 0;

Oy 3 QCHGNGQSTRGFTTGTCTGSSMTPHRQTPENYPNGLTMATCRPADTGP 62
Db 211 ECHTNGESYRGPDHTSGTCQRMQDQTPHRKFLPERYPDGFDNDGKRRP 270
Oy 63 WCFPTDPSIRMEYCNLRCS 82
Db 271 WCYTLDPDTPMEYCAIMCA 290

RESULT 14
HGFL_HUMAN STANDARD; PRT; 711 AA.
ID HGFL_HUMAN Q13350; Q14870;
AC P26927; Q13350; Q14870;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
DE stimulatory protein) (MSP) (Macrophage stimulating protein).
GN MST1 OR HGFL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=92002016; PubMed=1655021;
RA Han S., Stuart L.A., Flierer Degen S.J.;
RT "Characterization of the DNPI552 locus on human chromosome 3:
RT identification of a gene coding for four kringle domains with
RT homology to hepatocyte growth factor.";
RL Biochemistry 30:9768-9780(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=93340141; PubMed=8393443;
RA Yoshimura T., Yuhki N., Wang M.H., Leonard E.J.;
RT "Cloning, sequencing, and expression of human macrophage stimulating
RT protein (MSP, MST1) confirms MSP as a member of the family of kringle

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RT proteins and locates the MSP gene on chromosome 3.";
RL J. Biol. Chem. 268:15461-15468(1993).
CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
CC CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
CC CONSERVED.
CC -1- PTM: MAY BE CLEAVED AFTER AA 484, TO YIELD A TWO-CHAIN MOLECULE
CC HELD TOGETHER BY DISULFIDE BONDS, OR TWO SEPARATE POLYPEPTIDES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 4 kringle domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U74178; AAA50165.1; -
DR EMBL; U37055; AAC50471.1; -
DR EMBL; L11924; AAA59872.1; -
DR PIR; A40331; A47136.
DR HSR; P00747; 2PK4.
DR MEROPS; S01.975; -.
DR MIM; 142408; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR003966; Prochombin.
DR Pfam; PF00051; kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; KRingle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS50070; KRINGLE_2; 4.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
KW Kringle; Glycoprotein; Serine protease homolog; Repeat; Signal;
KW Polymorphism.
FT SIGNAL 1 18
FT CHAIN 19 711
FT DOMAIN 32 109
FT DOMAIN 110 186
FT DOMAIN 191 268
FT DOMAIN 283 361
FT DOMAIN 370 448
FT DOMAIN 484 711
FT DISULFID 56 78
FT DISULFID 60 66
FT DISULFID 110 186
FT DISULFID 131 169
FT DISULFID 157 181
FT DISULFID 191 268
FT DISULFID 194 324
FT DISULFID 212 251
FT DISULFID 240 263
FT DISULFID 283 361
FT DISULFID 304 343
FT DISULFID 332 355
FT DISULFID 370 448
FT DISULFID 391 431
FT DISULFID 419 443
FT DISULFID 468 588
FT DISULFID 507 523
FT DISULFID 602 667

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FT DISULFID 632 646 BY SIMILARITY.
 FT DISULFID 657 685 BY SIMILARITY.
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 13 13 Y -> C.
 FT VARIANT 212 212 /FTID=VAR_006631.
 FT VARIANT 212 212 C -> F.
 FT VARIANT 676 676 /FTID=VAR_006632.
 FT VARIANT 676 676 E -> K (IN DBSNP:7798).
 FT CONFLICT 623 623 /FTID=VAR_014569.
 FT CONFLICT 623 623 L -> F (IN REF. 2).
 SQ SEQUENCE: 711 AA; 80379 MW; 596ED21F180290B4 CRC64;
 Query Match 47.3%; Score 247.5; DB 1; Length 711;
 Best Local Similarity 50.6%; Pred. No. 4.6e-19;
 Matches 43; Conservative 13; Mismatches 28; Indels 1; Gaps 1;
 QY 2 ROCYHNGOSYRGTFSTTVGRTGTCOSWSMTPHRHQRTPEYVNDGLTMNYCRNPADT- 60
 DB 368 QDCYHNGEYRGTVSKTRGVCCQMSAFPHKPFITFSEPHAGLENFGRNPDCSH 427
 QY 61 GPCVFTTDSIRWEYCNLTRCSDE 85
 DB 428 GPCVFTTDSIRWEYCNLTRCSDE 85
 RESULT 15
 ID PLMN SHEEP STANDARD; PRT; 343 AA.
 AC P81286;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen (EC 3.4.21.7) (Fragment).
 GN Plg.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP MEDLINE=9314995; PubMed=1492092;
 RA Schaller J., Straub C., Kamfer U., Rickli E.E.;
 RT "Complete amino acid sequence of ovine miniplasminogen.";
 RL Protein Seq. Data Anal. 5:21-25(1992).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 higher selectivity than trypsin. Converts fibrin into soluble
 products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains at least 2 kringle domains.
 CC -1- SIMILARITY: Contains at least 2 kringle domains.
 DR HSSP: P00747; SHG.
 DR MEROPS: S01.233;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00051; kringle_1.

DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TRYPSIN; 1.
 DR PROSITE; PS00021; KRINGLE 1; 1.
 DR PROSITE; PS50070; KRINGLE 2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR HydroLase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
 FT NON_TER 1 1
 FT DOMAIN <1 140 HEAVY CHAIN A.
 FT DOMAIN 141 >343 LIGHT CHAIN A.
 FT DOMAIN <1 17 KRINGLE 4.
 FT DOMAIN 41 120 KRINGLE 5.
 FT ACT_SITE 114 341 SERINE PROTEASE.
 FT ACT_SITE 181 181 CHARGE RELAY SYSTEM.
 FT ACT_SITE 224 224 CHARGE RELAY SYSTEM.
 FT ACT_SITE 319 319 CHARGE RELAY SYSTEM.
 FT NON_TER 343 343
 SQ SEQUENCE 343 AA; 37662 MW; 8DF6BA92D596E0 CRC64;
 Query Match 44.7%; Score 234; DB 1; Length 343;
 Best Local Similarity 49.4%; Pred. No. 5.8e-18;
 Matches 41; Conservative 12; Mismatches 28; Indels 2; Gaps 2;
 QY 4 CYHNGOSYRGTFSTTVGRTGTCOSWSMTPHRHQRTPEYVNDGLTMNYCRNPADT- 61
 DB 15 CMLGIGKYRGKATTVAGVPCQEWAAQEPHRHGI FTETNPBAGLENGYCRNPDCVNG 74
 QY 62 PWCFTTDSIRWEYCNLTRCSDE 84
 DB 75 PWCFTTDSIRWEYCNLTRCSDE 84

Search completed: January 12, 2004, 17:23:57
 Job time : 7.69549 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:18:07 ; Search time 28.4398 Seconds
(without alignments)
807.553 Million cell updates/sec

Title: US-10-088-548-6
Perfect score: 523
Sequence: 1 VRQCHGNQSYRGFTSTV.....SIRWEYCNLTRCDTEGTV 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 517 | 98.9 | 113 | 4 Q9UR5 | Q9UR5 homo sapien |
| 2 | 485 | 92.7 | 454 | 6 O46506 | O46506 papio hamad |
| 3 | 444 | 84.9 | 810 | 4 Q15146 | Q15146 homo sapien |
| 4 | 439 | 83.9 | 132 | 4 O16609 | O16609 homo sapien |
| 5 | 413 | 79.0 | 113 | 4 Q9UR7 | Q9UR7 homo sapien |
| 6 | 408 | 78.0 | 105 | 4 Q9UR8 | Q9UR8 homo sapien |
| 7 | 405 | 77.4 | 113 | 4 Q9UR6 | Q9UR6 homo sapien |
| 8 | 404 | 77.2 | 359 | 6 Q8WNR1 | Q8WNR1 canis fam11 |
| 9 | 400 | 76.5 | 812 | 11 Q91WJ5 | Q91WJ5 mus musculu |
| 10 | 395 | 75.5 | 145 | 6 Q28911 | Q28911 macaca fasc |
| 11 | 379.5 | 72.6 | 812 | 11 Q980W3 | Q980W3 rattus norv |
| 12 | 360 | 68.8 | 806 | 6 O18783 | O18783 macropus eu |
| 13 | 303 | 57.9 | 2869 | 6 Q28398 | Q28398 erinaceus e |
| 14 | 281 | 53.7 | 429 | 13 Q8AVB0 | Q8AVB0 brachydanto |
| 15 | 272.5 | 52.1 | 716 | 11 Q91XG8 | Q91XG8 mus musculu |
| 16 | 268.5 | 51.3 | 709 | 13 Q902N6 | Q902N6 brachydanto |

| | | | | | |
|----|-------|------|-----|-----------|---------------------|
| 17 | 268.5 | 51.3 | 716 | 11 P70521 | P70521 rattus norv |
| 18 | 264 | 50.5 | 728 | 11 Q8C9G5 | Q8C9G5 mus musculu |
| 19 | 262 | 50.1 | 285 | 4 Q8CE2 | Q8CE2 homo sapien |
| 20 | 262 | 50.1 | 290 | 4 Q02935 | Q02935 homo sapien |
| 21 | 258 | 49.3 | 296 | 4 Q14519 | Q14519 homo sapien |
| 22 | 257.5 | 49.2 | 385 | 5 Q25101 | Q25101 herdamia m |
| 23 | 256.5 | 49.0 | 716 | 13 Q91691 | Q91691 xenopus lae |
| 24 | 256.5 | 49.0 | 728 | 6 Q9BH09 | Q9BH09 felis silve |
| 25 | 255.5 | 48.9 | 947 | 13 Q8AXY6 | Q8AXY6 gallus gall |
| 26 | 254 | 48.6 | 334 | 6 Q46507 | Q46507 papio hamad |
| 27 | 249.5 | 47.7 | 209 | 11 Q8BS17 | Q8BS17 mus musculu |
| 28 | 247.5 | 47.3 | 208 | 4 Q9BYM0 | Q9BYM0 homo sapien |
| 29 | 247.5 | 47.3 | 210 | 4 Q13494 | Q13494 homo sapien |
| 30 | 246.5 | 47.1 | 109 | 6 Q9N1B8 | Q9N1B8 ovis aries |
| 31 | 246.5 | 47.1 | 710 | 13 Q91402 | Q91402 xenopus lae |
| 32 | 246.5 | 47.1 | 717 | 13 P70006 | P70006 xenopus lae |
| 33 | 243.5 | 46.6 | 313 | 13 Q9PU78 | Q9PU78 crocodylus |
| 34 | 243.5 | 46.6 | 567 | 4 Q13208 | Q13208 homo sapien |
| 35 | 243.5 | 46.6 | 948 | 5 Q9Y1Y6 | Q9Y1Y6 ephydactia f |
| 36 | 242 | 46.3 | 726 | 13 Q90978 | Q90978 gallus gall |
| 37 | 241.5 | 46.2 | 211 | 11 Q55027 | Q55027 mus musculu |
| 38 | 241.5 | 46.2 | 215 | 13 Q42341 | Q42341 gallus gall |
| 39 | 239.5 | 45.8 | 704 | 13 Q90865 | Q90865 gallus gall |
| 40 | 237.5 | 45.4 | 946 | 13 Q07153 | Q07153 torpedo cal |
| 41 | 232.5 | 44.5 | 648 | 4 Q9H1V4 | Q9H1V4 homo sapien |
| 42 | 223 | 42.6 | 53 | 4 Q9UM12 | Q9UM12 homo sapien |
| 43 | 223 | 42.6 | 95 | 4 Q8N696 | Q8N696 homo sapien |
| 44 | 220.5 | 42.2 | 930 | 13 Q8AV69 | Q8AV69 xenopus lae |
| 45 | 212.5 | 40.6 | 801 | 11 Q8K0Q8 | Q8K0Q8 mus musculu |

ALIGNMENTS

RESULT 1
Q9UR5 PRELIMINARY; PRT; 113 AA.
ID Q9UR5
AC Q9UR5; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DT Apo1ipoprotein(a) (Fragment).
GN APOA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2181705; PubMed=11285247;
RA Ogorelkova M., Kraft H.G., Ehnholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV
RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
RT different patterns in Africans and Caucasians";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -1- SIMILARITY: CONTRAINS 1 KRINGLE DOMAIN.
DR EMBL; AF158663; AA03680.1; JOINED.
DR EMBL; AF158662; AA03680.1; JOINED.
DR HSSP; P00747; IPWK.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
KW Glycoprotein; Kringle; Lipoprotein.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12685 MW; F3D65681D9B5253A CRC64;
Query Match 98.9%; Score 517; DB 4; Length 113;
Best Local Similarity 98.9%; Pred. No. 1.7e-52;

Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRQCYHNGGSGYRGFTSTVTGRTCCSSMTPHRRQTPENYPNDGLTMNYCRNPADDT 60
 DB 8 VRQCYHNGGSGYRGFTSTVTGRTCCSSMTPHRRQTPENYPNDGLTMNYCRNPADDT 67
 QY 61 GPWCFTTDPSSIRMEYCNLTRCSDTEGTVV 89
 DB 68 GPWCFTTDPSSIRMEYCNLTRCSDTEGTVV 96

RESULT 2
 046506 PRELIMINARY; PRT; 454 AA.

AC 046506;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Apolipoprotein a (Fragment).
 GN BABAOA.
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OC NCBI_TaxId=9557;
 OX NCBI_TaxId=9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cox U.A., Jett C., Hixson J.E.,
 RT "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
 RT Site Mutation is Associated with Deletion of a Single Exon in a Null
 RT Allele."
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC EMBL; AF029691; AAB97886.1; -.
 DR HSSP; P00747; 2PK4.
 DR MEROPS; S01.999; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00051; Kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; TRY_P_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS00070; KRINGLE_2; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Glycoprotein; Hydroxylase; Lipoprotein; Protease;
 KW Serine protease.
 KM NON TER
 FT 1 1
 SO SEQUENCE 454 AA; 50041 MW; 974E30744C187B2F CRC64;

Query Match 92.7%; Score 485; DB 6; Length 454;
 Best Local Similarity 89.9%; Pred. No. 4.2e-46;
 Matches 80; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 VRQCYHNGGSGYRGFTSTVTGRTCCSSMTPHRRQTPENYPNDGLTMNYCRNPADDT 60
 DB 99 VRQCYHNGGSGYRGFTSTVTGRTCCSSMTPHRRQTPENYPNDGLTMNYCRNPADDT 158
 QY 61 GPWCFTTDPSSIRMEYCNLTRCSDTEGTVV 89
 DB 159 GPWCFTTDPSSIRMEYCNLTRCSDTEGTVV 187

RESULT 3
 015146 PRELIMINARY; PRT; 810 AA.
 AC 015146;

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Plasminogen precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue=Liver;
 RA Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
 RA Mitchell D., Robinson J.H.;
 RT "Expression of recombinant human plasminogen and aglycoplasminogen in
 RT HeLa cells."
 RL Fibrinolysis 0.0-0.0(1991).
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 CC EMBL; M74220; AAA6451.1; -.
 DR HSSP; P00747; 2PK4.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRY_P_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein; Hydroxylase; Protease; Serine protease; Signal.
 FT SIGNAL
 FT CHAIN 1 19 POTENTIAL.
 FT 20 810 PLASMOGEN.
 SO SEQUENCE 810 AA; 90555 MW; B05C7D4B0D020B3C CRC64;

Query Match 84.9%; Score 444; DB 4; Length 810;
 Best Local Similarity 82.0%; Pred. No. 4.7e-43;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRQCYHNGGSGYRGFTSTVTGRTCCSSMTPHRRQTPENYPNDGLTMNYCRNPADDT 60
 DB 374 VRQCYHNGGSGYRGFTSTVTGRTCCSSMTPHRRQTPENYPNDGLTMNYCRNPADDT 433
 QY 61 GPWCFTTDPSSIRMEYCNLTRCSDTEGTVV 89
 DB 434 GPWCFTTDPSSIRMEYCNLTRCSDTEGTVV 462

RESULT 4
 016609 PRELIMINARY; PRT; 132 AA.
 ID 016609;
 AC 016609;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE (APOARGC).
 GN APOARGC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Liver;
 RX MEDLINE=95268939; PubMed=7749817;
 RA Byrne C.D., Schwartz K., Lawn R.M.;
 RT "Loss of a splice donor site at a 'skipped exon' in a gene homologous
 to apolipoprotein(a) leads to an mRNA encoding a protein consisting of
 a single kringle domain."
 RL Arterioscler. Thromb. Vasc. Biol. 15:65-70(1995).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL: U9517; AA85693.1; -;
 DR EMBL: U9517; AA85692.1; -;
 DR HSSP: P00747; 1PK.
 DR InterPro: IPR000001; Kringle.
 DR Pfam: PF00051; kringle; 1.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000395; Kringle; 1.
 DR SMART: SM00130; KR; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 KW Glycoprotein; Kringle.
 SQ SEQUENCE 132 AA; 1486 MW; 3794AD30A586DBA CRC64;

Query Match 83.9%; Score 439; DB 4; Length 132;
 Best Local Similarity 79.5%; Pred. No. 2,4e-43;
 Matches 70; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 VROCYHNGSGSYRGFTSTVTGRTQSSWSMTPHRHQRTPEYVNDGLTMYCRNPDDT 60
 DB 25 VQDCHNGSGSYRGFTSTVTGRTQSSWSMTPHRHQRTPEYVNDGLTMYCRNPDDT 84
 QY 61 GPWCFTDPSIRMEYCNLTRCSDTGTV 88
 DB 85 GPWCYTTDPNVMEYCNLTRCSDEGTV 112

RESULT 5

ID Q9UR7 PRELIMINARY; PRT; 113 AA.

AC Q9UR7;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (Fragment).

GN APOA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21181705; PubMed=11285247;
 RA Ogorelko M., Kraft H.G., Rhinholm C., Utermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV
 types 6 to 10 domain affect Lp(a) plasma concentrations and have
 RT different patterns in Africans and Caucasians."
 RL Hum. Mol. Genet. 10:815-824(2001).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL: AF158659; AAF03678.1; -;
 DR EMBL: AF158658; AAF03678.1; JOINED.
 DR HSSP: P00747; 2PK4.
 DR InterPro: IPR000001; Kringle.
 DR Pfam: PF00051; kringle; 1.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000395; Kringle; 1.
 DR SMART: SM00130; KR; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 KW Glycoprotein; Kringle; Lipoprotein.
 FT NON_TER 1
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12815 MW; 4F80ADP8708548CB CRC64;

Query Match 79.0%; Score 413; DB 4; Length 113;
 Best Local Similarity 77.5%; Pred. No. 2.1e-40;

Matches 69; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 VROCYHNGSGSYRGFTSTVTGRTQSSWSMTPHRHQRTPEYVNDGLTMYCRNPDDT 60
 DB 8 VQDCHNGSGSYRGFTSTVTGRTQSSWSMTPHRHQRTPEYVNDGLTMYCRNPDDT 67
 QY 61 GPWCFTDPSIRMEYCNLTRCSDTGTV 89
 DB 68 GPWCYTTDPNVMEYCNLTRCSDEGTV 96

RESULT 6

ID Q9UR8 PRELIMINARY; PRT; 105 AA.

AC Q9UR8;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (Fragment).

GN APOA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21181705; PubMed=11285247;
 RA Ogorelko M., Kraft H.G., Rhinholm C., Utermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV
 types 6 to 10 domain affect Lp(a) plasma concentrations and have
 RT different patterns in Africans and Caucasians."
 RL Hum. Mol. Genet. 10:815-824(2001).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL: AF158656; AAF03677.1; -;
 DR EMBL: AF158655; AAF03677.1; JOINED.
 DR HSSP: P00747; 2PK4.
 DR InterPro: IPR000001; Kringle.
 DR Pfam: PF00051; kringle; 1.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000395; Kringle; 1.
 DR SMART: SM00130; KR; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 KW Glycoprotein; Kringle; Lipoprotein.

FT NON_TER 1
 FT NON_TER 105
 SQ SEQUENCE 105 AA; 11882 MW; 6ECB6C02CD30EFA2 CRC64;
 Query Match 78.0%; Score 408; DB 4; Length 105;
 Best Local Similarity 75.3%; Pred. No. 7,4e-40;
 Matches 67; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 VROCYHNGSGSYRGFTSTVTGRTQSSWSMTPHRHQRTPEYVNDGLTMYCRNPDDT 60
 DB 8 VQDCHNGSGSYRGFTSTVTGRTQSSWSMTPHRHQRTPEYVNDGLTMYCRNPDDT 67
 QY 61 GPWCFTDPSIRMEYCNLTRCSDTGTV 89
 DB 68 GPWCYTTDPNVMEYCNLTRCSDEGTV 96

RESULT 7

ID Q9UR6 PRELIMINARY; PRT; 113 AA.

AC Q9UR6;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (Fragment).

GN APOA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OX  NCBI_TaxId=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=2181705; PubMed=11285247;
RA  Ogorelkova M., Kraft H.G., Enholm C., Utermann G.;
RT  "Single nucleotide polymorphisms in exons of the apo(a) kringle IV
RT  types 6 to 10 domain affect Lp(a) plasma concentrations and have
RT  different patterns in Africans and Caucasians.";
RL  Hum. Mol. Genet. 10:815-824(2001).
CC  -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR  EMBL; AF158661; AF03679.1; -.
DR  HSSP; P00747; 2PK4.
DR  InterPro; IPR000001; Kringle.
DR  Pfam; PF00051; Kringle.1.
DR  PRINTS; PR00018; KRINGLE.
DR  ProDom; PD000395; Kringle.1.
DR  SMART; SM00130; KR; 1.
DR  PROSITE; PS00021; KRINGLE_1; 1.
DR  PROSITE; PS00070; KRINGLE_2; 1.
KM  Glycoprotein; Kringle; Lipoprotein.
FT  NON_TER 1
FT  NON_TER 1
SQ  SEQUENCE 113 AA; 12697 MW; 51D4461D9C6312E CRC64;

Query Match 77.4%; Score 405; DB 4; Length 113;
Best Local Similarity 75.3%; Pred. No. 1.8e-39;
Matches 67; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 1 VROCHNGGOSYRGSTSTVTGRTCSWSSMTPHRHQRTPENYVNDGLTNNYCRNPADAT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 8 VQDCYHGDGSRYSIGISSTITVTGRTCSWSSMTPHRHQRTPENYVNDGLTNNYCRNPADGK 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 GPMCFITDPSIRWEYCNLTGCSDEGTIV 89
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 68 QPMCYTTPCVRWEYCNLTGCSDEGTIV 96
   |||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
OQWNR1 PRELIMINARY; PRT; 359 AA.
ID OQWNR1;
AC OQWNR1;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE PlasmaInogen (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Pyle-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kieker O.,
RA Folkman J., Waters D.J.;
RT "Angiotensin is detectable in the urine of dogs with spontaneous Bone
RT Cancer.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR EMBL; AY069985; AAL58519.1; -.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003966; Prothrombin.
DR Pfam; PF00051; Kringle.4.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle.4.
DR SMART; SM00130; KR; 4.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS00070; KRINGLE_2; 4.
KM Glycoprotein; Kringle.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 359 AA; 41172 MW; 776D35FAAB0BD9E CRC64;

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Query Match 77.2%; Score 404; DB 6; Length 359;
Best Local Similarity 77.8%; Pred. No. 8.5e-39;
Matches 63; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

OY 1 VROCHNGGOSYRGSTSTVTGRTCSWSSMTPHRHQRTPENYVNDGLTNNYCRNPADAT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 279 VQDCYHGDGSRYSIGISSTITVTGRTCSWSSMTPHRHQRTPENYVNDGLTNNYCRNPADGK 338
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 GPMCFITDPSIRWEYCNLTGCSDEGTIV 81
   |||:|||||:|||||:|||||:|||||:|||||:
DB 339 SPWCYTTPCVRWEYCNLTGCSDEGTIV 359
   |||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
OQ1WJ5 PRELIMINARY; PRT; 812 AA.
ID OQ1WJ5;
AC OQ1WJ5;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE PlasmaInogen.
GN Plg.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Liver;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv.
RA Bratwalte M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
RA Nagaraja R.;
RT "Genomic Sequence Analysis in the Mouse t-complex Region.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL; BC014773; AA14773.1; -.
DR EMBL; AF481053; AA22156.1; -.
DR HSSP; P00761; 1AN1.
DR MGD; MGI:97620; Plg.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00051; Kringle.5.
DR Pfam; PF00024; PAN.1.
DR Pfam; PF00089; trypsin.1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle.5.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 812 AA; 90781 MW; 24173260E6A2FFD2 CRC64;

Query Match 76.5%; Score 400; DB 11; Length 812;
Best Local Similarity 70.8%; Pred. No. 6.2e-38;
Matches 63; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

OY 1 VROCHNGGOSYRGSTSTVTGRTCSWSSMTPHRHQRTPENYVNDGLTNNYCRNPADAT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 374 VQDCYHGDGSRYSIGISSTITVTGRTCSWSSMTPHRHQRTPENYVNDGLTNNYCRNPADGK 433
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 61 GPMCFITDPSIRMEYCNLTRCSDTEGTV 89
DB 434 GPMCFITDPSIRMEYCNLTRCSDTEGTV 462

RESULT 10
Q28911 PRELIMINARY; PRT; 145 AA.
ID 028911
AC 028911;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
GN Apolipoprotein(a) (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
NCBI_TaxID=9541;
RN (1)
RX MEDLINE=9539387; PubMed=7666007;
RA Ramnarack R., Spahr M.A., Hicks G.W., Kieft K.A., Brammer D.W.,
RA Minton L.L.; Newton R.S.;
RT "Gemfibrozil significantly lowers cynomolgus monkey plasma
RT lipoprotein(a)-protein and liver apolipoprotein(a) mRNA levels.";
RL J. Lipid Res. 36:1294-1304(1995).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; S79621; AAD14312.1; -.
DR HSSP; P00747; 2PKA.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR KW Glycoprotein; Kringle; Lipoprotein.
FT NON TER 145
SQ SEQUENCE 145 AA; 16097 MW; 0D2DA20A06A5D87 CRC64;

Query Match 75.5%; Score 395; DB 6; Length 145;
Best Local Similarity 73.0%; Pred. No. 3.4e-38;
Matches 65; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 VROCHNGSGYRGFTSTVTGRTQSGSSMTPHRQRTPEYPNGLTMYNCRPDDAT 60
DB 40 VDDCYHGDQSYOGTSTVTGRTQAWSMBPHQNRRTENYPNAGLIRNYCRNPDPVA 99
QY 61 GPMCFITDPSIRMEYCNLTRCSDTEGTV 89
DB 100 APCTYMDPVRMEYCNLTRCSDAEGTAV 128

RESULT 11
Q9R0W3 PRELIMINARY; PRT; 812 AA.
ID Q9R0W3
AC Q9R0W3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Plasminogen protein precursor (EC 3.4.21.7).
OS PLASMINOGEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN (1)
RX SEQUENCE FROM N.A.
RA TISSUE=Liver;
RA Bangert K., Johnsen A.H., Thorsen S.;
RT "Rat plasminogen: cDNA and gene structure.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

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RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91250378; PubMed=1645711;
RA Kanalas J.U., Makker S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
RT receptor site for plasminogen.";
RL J. Biol. Chem. 266:10825-10829(1991).
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL; AJ242649; CAB46014.1; -.
DR HSSP; P00747; 1PMK.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan app.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR001400; Somatostatin.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00338; SOMATOSTATIN_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR KW Glycoprotein; Hydrolyase; Kringle; Protease; Serine protease; Signal.
FT SIGNAL 1
FT CHAIN 1
SQ SEQUENCE 812 AA; 90535 MW; 8C703C51410BEC9E CRC64;

Query Match 72.6%; Score 379.5; DB 11; Length 812;
Best Local Similarity 71.9%; Pred. No. 1.5e-35;
Matches 64; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 VROCHNGSGYRGFTSTVTGRTQSGSSMTPHRQRTPEYPNGLTMYNCRPDDAD 59
DB 373 VOECTQNGKSYRGFTSTVTGRTQKQSVSMTHPSHSTKTPANFPDAGLMMYCNCRNPDDQ 432
QY 60 TGPWCFTDPSIRMEYCNLTRCSDTEGTV 88
DB 433 GPMCFITDPSIRMEYCNLTRCSDTEGTV 461

RESULT 12
O18783 PRELIMINARY; PRT; 806 AA.
ID O18783
AC O18783;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Plasminogen.
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TaxID=9315;
RN (1)
RX SEQUENCE FROM N.A.
RA TISSUE=Liver;
RA MEDLINE=98004511; PubMed=9342350;
RA Lawn R.M., Schwartz K., Patchy L.;
RT "Convergent evolution of apolipoprotein(a) in primates and hedgehog.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL; AF012297; AAB65760.1; -.

```

DR HSP; P00747; SHPG.
 DR MEROPS; S01.233; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringles.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser protease_Try.
 DR Pfam; PF00051; Kringles; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringles; 5.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR GlycoProfile; Hydrolase; Kringles; Protease; Serine protease.
 KM SEQUENCE 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;

Query Match 68.8%; Score 360; DB 6; Length 806;
 Best Local Similarity 59.6%; Pred. No. 2.7e-33; Matches 53; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

Qy 1 VROCYNHNGOSYRGTFSTVTYTGRTQGSWSMTPHRHQRTPENTYNDGLTMNYCRNPADT 60
 Db 368 IQCEBKSGKNYGTSTTISGKKQCAWSSMTPHQHKTDNPNMDLINYCRNPDK 427
 Qy 61 GPCWCTTDPSSIRMEYCNLTGCSDEGTIV 89
 Db 428 SPCWCTMDPTVRWEFCNLEKSCGTGTVL 456

RESULT 13
 Q28398 PRELIMINARY; PRT; 2869 AA.
 AC Q28398;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (Fragment).
 OS Brinaceus europaeus (Western European hedgehog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
 NCBI_TaxId=9365;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96025778; PubMed=7592597;
 RA Lavin R.M., Boommark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
 BA Byrne C.D., Pong K.J., Meer K., Patchy L.;
 RT "The recurring evolution of lipoprotein(a). Insights from cloning of
 RT hedgehog apolipoprotein(a).";
 RL J. Biol. Chem. 270:24004-24009(1995).
 CC -1- SIMILARITY: CONTAINS 31 KRINGLE DOMAINS.
 DR EMBL; U03170; AAC48522.1; -.
 DR HSP; P00747; SHPG.
 DR InterPro; IPR000001; Kringles.
 DR Pfam; PF00051; Kringles; 31.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringles; 31.
 DR SMART; SM00130; KR; 31.
 DR PROSITE; PS00021; KRINGLE_1; 30.
 DR PROSITE; PS00070; KRINGLE_2; 31.
 DR GlycoProfile; Kringles; Lipoprotein.
 KM SEQUENCE 2869 AA; 318601 MW; 9527CEP985A4FB2A CRC64;
 FT NON TER 1

Query Match 57.9%; Score 303; DB 6; Length 2869;
 Best Local Similarity 58.2%; Pred. No. 4.8e-26; Matches 46; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

Qy 3 OCHYHNGOSYRGTFSTVTYTGRTQGSWSMTPHRHQRTPENTYNDGLTMNYCRNPADT 62
 Db 2776 OCLKNGESYQGNISVSGYTCORWREQTPRHARTPDNYPCKNLVGNVCRNPDEAVP 2835
 Qy 63 WCFTTDPSSIRMEYCNLTGCSDEGTIV 81
 Db 2836 WCFTTSAVRMEYCSIPTC 2854

RESULT 14
 Q28398 PRELIMINARY; PRT; 429 AA.
 AC Q28398;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Plasminogen precursor (Fragment).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hanumanthiah R., Day K., Jagadeeswaran P.;
 RT "Comprehensive analysis of blood coagulation pathways in teleostei:
 RT Evolution of coagulation factor genes and identification of zebrafish
 RT factor VIIa.";
 RL Blood Cells Mol. Dis. 0:0-0(2002).
 DR EMBL; AF515276; AAN71006.1; -.
 FT NON TER 1
 SQ SEQUENCE 429 AA; 47556 MW; 9A580A21A549C12 CRC64;

Query Match 53.7%; Score 281; DB 13; Length 429;
 Best Local Similarity 57.3%; Pred. No. 2.1e-24; Matches 47; Conservative 12; Mismatches 21; Indels 2; Gaps 2;

Qy 2 RQCHNGOSYRGTFSTVTYTGRTQGSWSMTPHRHQRTPENTYNDGLTMNYCRNPADT 59
 Db 100 KCKKNGAEGYSGTSMYGVYCOAWRSMTPHQAFTPEHPDKGLSNOCRNPDSDV 159
 Qy 60 TGPWCTTDPSSIRMEYCNLTGCSDEGTIV 81
 Db 160 NGPWCTTDPSSIRMEYCNLTGCSDEGTIV 181

RESULT 15
 Q28398 PRELIMINARY; PRT; 716 AA.
 AC Q28398;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hepatocyte growth factor-like.
 GN HGF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 DR EMBL; BC010551; AAH10551.1; -.
 DR HSP; P00761; IAN1.
 DR MGD; MGI:96080; Hgfl.

DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003603; Pan_app.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO1505; PROTHROMBIN.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS50070; KRINGLE_2; 4.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KM Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 716 AA; 80693 MW; 12474C48A7D4B46D CRC64;

Query Match 52.1%; Score 272.5; DB 11; Length 716;
Best Local Similarity 55.4%; Pred. No. 3.6e-23;
Matches 46; Conservative 11; Mismatches 25; Indels 1; Gaps 1;

QY 4 CYHNGQSYRGCTSTVTGRTCSMSMTPRHQRTPENTPNDGLTMYCRNPDAAT-GP 62
DB 379 CYHSGEQYRGVSVKTRKGVQCOHWSSETPHKPQFTPTSAPOAGLEANFCRNPDSGSHGP 438
QY 63 WCFETDPSIRWEYCNLTRCSDE 85
DB 439 WCYTLDPDILFDYCALQRCDDQ 461

Search completed: January 12, 2004, 17:25:37
Job time : 28.4398 secs

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XX Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
 PT diseases, e.g. cancer and rheumatoid arthritis, has human
 PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
 PT sequence -
 PS Claim 2; Page 45-46; 50pp; English.

XX The present sequence is human LK7 protein which contains the amino
 CC acid sequence of human apolipoprotein(a) kringle domain IV37
 CC (KIV37). The human apolipoprotein(a) kringle domains IV36 (LK6
 CC protein), IV37 (LK7 protein) and V38 (LK8 protein) together form the
 CC angiogenesis inhibitor, LK68 protein. LK68, LK6, LK7 and LK8 are
 CC inhibitors are of endothelial cell proliferation, cell migration and
 CC normal development of capillaries in the chick embryo chorioallantoic
 CC membrane (CAM). LK68 protein, its single kringles or their functional
 CC equivalents, are useful for treating angiogenesis-mediated diseases,
 CC such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic
 CC disease in animals or humans. LK68 is useful as an anticancer agent and
 CC also for inhibiting primary tumour growth.

XX Sequence 89 AA;
 SQ

Query Match 100.0%; Score 523; DB 22; Length 89;
 Best Local Similarity 100.0%; Pred. No. 5.2e-46;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRQCHNGQSYRGFTSTVTGRTCSWSMTPHRHQRTPENPNGLTMNYCRNPDAOT 60
 DB 1 VRQCHNGQSYRGFTSTVTGRTCSWSMTPHRHQRTPENPNGLTMNYCRNPDAOT 60
 QY 61 GPMCFITDPSIRMEYCNLTRCSDTEGTV 89
 DB 61 GPMCFITDPSIRMEYCNLTRCSDTEGTV 89

RESULT 2
 AAY72944
 ID AAY72944 standard; Protein; 308 AA.
 AC AAY72944;
 XX
 DT 13-JUN-2001 (first entry)
 XX

DE Human angiogenesis inhibitor, LK68 protein.
 XX
 KM Human; angiogenesis inhibitor; LK68; apolipoprotein(a) kringle domain;
 KM angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy;
 KM cytostatic; antirheumatic; antiarthritic; antiproliferative; psoriasis;
 KM ocular angiogenic disease; endothelial cell proliferation; tumour;
 KM cell migration.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key location/Qualifiers
 FT Domain 1..91
 FT /label= KIV36
 FT /note= "Apolipoprotein(a) kringle domain IV36, LK6
 FT protein"
 FT Domain 119..207
 FT /label= KIV37
 FT /note= "Apolipoprotein(a) kringle domain IV37, LK7
 FT protein"
 FT Domain 223..308
 FT /label= KV38
 FT /note= "Apolipoprotein(a) kringle domain V38, LK8
 FT protein"
 XX
 PN WO200119868-A1.
 XX
 PD 22-MAR-2001.
 XX
 PF 15-SEP-1999; 99WO-KR00554.

XX 15-SEP-1999; 99WO-KR00554.
 PR
 XX (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
 PA
 XX Chang J, Kim JS, Park EJ, Yum J, Chung S;
 PI
 XX WPI; 2001-24787/25.
 DR N-PSDB; AAD03255.
 XX

PT Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
 PT diseases, e.g. cancer and rheumatoid arthritis, has human
 PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
 PT sequence -
 PS Claim 4; Page 42-44; 50pp; English.

XX The present sequence is human angiogenesis inhibitor, LK68 protein.
 CC LK68 protein contains the amino acid sequences of human apolipoprotein(a)
 CC kringle domains IV36 (LK6 protein), IV37 (LK7 protein) and V38
 CC (LK8 protein). LK68, LK6, LK7 and LK8 are inhibitors are of endothelial
 CC cell proliferation, cell migration and normal development of capillaries
 CC in the chick embryo chorioallantoic membrane (CAM). LK68 protein, its
 CC single kringles or their functional equivalents, are useful for
 CC treating angiogenesis-mediated diseases, such as cancer, rheumatoid
 CC arthritis, psoriasis or ocular angiogenic disease in animals or humans.
 CC LK68 is useful as an anticancer agent and also for inhibiting primary
 CC tumour growth.

XX Sequence 308 AA;
 SQ

Query Match 100.0%; Score 523; DB 22; Length 308;
 Best Local Similarity 100.0%; Pred. No. 2e-45;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRQCHNGQSYRGFTSTVTGRTCSWSMTPHRHQRTPENPNGLTMNYCRNPDAOT 60
 DB 119 VRQCHNGQSYRGFTSTVTGRTCSWSMTPHRHQRTPENPNGLTMNYCRNPDAOT 178
 QY 61 GPMCFITDPSIRMEYCNLTRCSDTEGTV 89
 DB 179 GPMCFITDPSIRMEYCNLTRCSDTEGTV 207

RESULT 3
 AAB01909
 ID AAB01909 standard; Protein; 90 AA.
 AC AAB01909;
 XX
 DT 18-SEP-2000 (first entry)
 XX

DE Human plasminogen kringle 4 (Val354-Val443).
 XX
 KM Plasminogen; human; kringle domain; endothelial cell proliferation;
 KM angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
 KM antiproliferative; antiproliferative; antiproliferative; antiproliferative;
 KM antiproliferative; antiproliferative; antiproliferative; antiproliferative;
 KM antiproliferative; cancer; tumour; autoimmune disease.
 XX
 OS Homo sapiens.
 XX
 PN US6057122-A.
 XX
 PD 02-MAY-2000.
 XX
 PF 05-MAY-1997; 97US-0851350.
 XX
 PR 03-MAY-1996; 96US-0643219.
 PR 03-APR-1997; 97US-0832087.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Davidson DJ;

XX WPI; 2000-349573/30.

XX Preparation of Kringles five peptide fragment for treating various
XX disorders such as angiogenic, ocular, skin diseases and cancer,
XX involves mixing mammalian plasminogen and elastase followed by
XX incubation and isolation -

XX Example 17; Page -; 48pp; English.

XX The invention relates to a method of preparing plasminogen kringles 5
XX peptide fragments. The method comprises mixing mammalian plasminogen and
XX elastase in the ratio 1:100-1:300, followed by incubating and isolating
XX the fragment. The kringles 5 peptides are inhibitors of angiogenesis and
XX endothelial cell proliferation and migration. The peptides are useful
XX for treating angiogenic diseases, primary and metastatic solid tumours
XX and carcinomas of various organs such as breast, genital tract,
XX endocrine glands, skin, tumours of the brain and eyes and solid tumours
XX arising from haematopoietic malignancies such as leukaemias and
XX lymphomas. They are also used for the prophylaxis of various autoimmune
XX diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
XX (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
XX Syndrome), diseases caused by excessive or abnormal stimulation of
XX endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
XX which have angiogenesis as a pathologic consequence (e.g., cat scratch
XX disease and ulcers). The peptides are also useful as a birth control
XX agent which inhibits ovulation and establishment of the placenta.
XX Sequences AAB01906-B01919 represent fragments of human plasminogen used
XX in an exemplification of the invention.
XX Note: This sequence is not shown in the specification, but is derived
XX from the full length human plasminogen sequence (AAB01887) shown in
XX figure 1.

XX Sequence 90 AA;

Query Match 84.9%; Score 444; DB 21; Length 90;
Best Local Similarity 82.0%; Pred. No. 6.2e-38;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VROCHGNGSGYRGFTSTVTGRTQSSMSMTPHRQRTPEYNDGLTMNYCRNPADT 60
DB 2 VDDCYHGDGSGYRGFTSTVTGRTQSSMSMTPHRQRTPEYNDGLTMNYCRNPADT 61

QY 61 GPMCFITDPSIRWEXCNLTRCSDEGTGV 89
DB 62 GPMCFITDPSIRWEXCNLTRCSDEGTGV 90

RESULT 4

AAB01918 standard; Protein; 189 AA.

AC AAB01918;

DT 18-SEP-2000 (first entry)

XX Human plasminogen kringles 4-5 (Val355-Ala543).

XX plasminogen; human; kringles domain; endothelial cell proliferation;
XX angiogenesis; antiproliferative; antiarteriosclerotic; cyostatic;
XX antiapoptotic; antiinflammatory; anticancer; antirheumatic; antiarthritic;
XX antiangiogenic; cancer; tumour; autoimmune disease.

XX Homo sapiens.

XX US6057122-A.

XX 02-MAY-2000.

XX 05-MAY-1997; 97US-0851350.

XX 03-MAY-1996; 96US-0643219.
XX 03-APR-1997; 97US-0832087.

XX (ABBO) ABBOTT LAB.

XX Davidson DJ;

XX WPI; 2000-349573/30.

XX Preparation of Kringles five peptide fragment for treating various
XX disorders such as angiogenic, ocular, skin diseases and cancer,
XX involves mixing mammalian plasminogen and elastase followed by
XX incubation and isolation -

XX Example 17; Page -; 48pp; English.

XX The invention relates to a method of preparing plasminogen kringles 5
XX peptide fragments. The method comprises mixing mammalian plasminogen and
XX elastase in the ratio 1:100-1:300, followed by incubating and isolating
XX the fragment. The kringles 5 peptides are inhibitors of angiogenesis and
XX endothelial cell proliferation and migration. The peptides are useful
XX for treating angiogenic diseases, primary and metastatic solid tumours
XX and carcinomas of various organs such as breast, genital tract,
XX endocrine glands, skin, tumours of the brain and eyes and solid tumours
XX arising from haematopoietic malignancies such as leukaemias and
XX lymphomas. They are also used for the prophylaxis of various autoimmune
XX diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
XX (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
XX Syndrome), diseases caused by excessive or abnormal stimulation of
XX endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
XX which have angiogenesis as a pathologic consequence (e.g., cat scratch
XX disease and ulcers). The peptides are also useful as a birth control
XX agent which inhibits ovulation and establishment of the placenta.
XX Sequences AAB01906-B01919 represent fragments of human plasminogen used
XX in an exemplification of the invention.
XX Note: This sequence is not shown in the specification, but is derived
XX from the full length human plasminogen sequence (AAB01887) shown in
XX figure 1.

XX Sequence 189 AA;

Query Match 84.9%; Score 444; DB 21; Length 189;
Best Local Similarity 82.0%; Pred. No. 1.4e-37;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VROCHGNGSGYRGFTSTVTGRTQSSMSMTPHRQRTPEYNDGLTMNYCRNPADT 60
DB 1 VDDCYHGDGSGYRGFTSTVTGRTQSSMSMTPHRQRTPEYNDGLTMNYCRNPADT 60

QY 61 GPMCFITDPSIRWEXCNLTRCSDEGTGV 89
DB 61 GPMCFITDPSIRWEXCNLTRCSDEGTGV 89

RESULT 5

AAB01919 standard; Protein; 192 AA.

AC AAB01919;

DT 18-SEP-2000 (first entry)

XX Human plasminogen kringles 4-5 (Val355-Phe546).

XX plasminogen; human; kringles domain; endothelial cell proliferation;
XX angiogenesis; antiproliferative; antiarteriosclerotic; cyostatic;
XX antiapoptotic; antiinflammatory; anticancer; antirheumatic; antiarthritic;
XX antiangiogenic; cancer; tumour; autoimmune disease.

XX Homo sapiens.

XX US6057122-A.

XX 02-MAY-2000.

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PF 05-MAY-1997; 97US-0851350.
PR 03-MAY-1996; 96US-0643219.
PR 03-APR-1997; 97US-0832087.
PA (ABBO ) ABBOTT LAB.
PI Davidson DJ;
XX WPI; 2000-349573/30.
XX
XX Preparation of Kringle five peptide fragment for treating various
XX disorders such as angiogenic, ocular, skin diseases and cancer,
XX involves mixing mammalian plasminogen and elastase followed by
XX incubation -
XX
XX Example 17; Page -: 48pp; English.
XX
XX The invention relates to a method of preparing plasminogen kringle 5
XX and peptide fragments. The method comprises mixing mammalian plasminogen and
XX elastase in the ratio 1:100-1:300, followed by incubating and isolating
XX the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
XX endothelial cell proliferation and migration. The peptides are useful
XX for treating angiogenic diseases, primary and metastatic solid tumours
XX and carcinomas of various organs such as breast, genital tract,
XX endocrine glands, skin, tumours of the brain and eyes and solid tumours
XX arising from haematopoietic malignancies such as leukaemias and
XX lymphomas. They are also used for the prophylaxis of various autoimmune
XX diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
XX (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
XX Syndrome), diseases caused by excessive or abnormal stimulation of
XX endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
XX which have angiogenesis as a pathologic consequence (e.g., cat scratch
XX disease and ulcers). The peptides are also useful as a birth control
XX agent which inhibits ovulation and establishment of the placenta.
XX Sequences AAB01906-801919 represent fragments of human plasminogen used
XX in an exemplification of the invention.
XX Note: This sequence is not shown in the specification, but is derived
XX from the full length human plasminogen sequence (AAB01887) shown in
XX figure 1.
XX
XX Sequence 192 AA;
SQ
XX
XX Query Match 84.9%; Score 444; DB 21; Length 192;
XX Best Local Similarity 82.0%; Pred. No. 1.4e-37;
XX Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
OY 1 VROCCHNGGSGYRGFFSTVTVGRTGQSSNSTPRHQSTPPNYPDGLTMNYCNPDDT 60
DB 1 VODCHGSGGSGYRGSSSTTTGGKKQSSSMTPRHQSTPPNYPAGLTMNYCNPDDK 60
OY 61 GPMCFPTDPSIRWEXCNLTGCSDETEGVV 89
DB 61 GPMCFPTDPSYRWEXCNLTGCSDETEGVV 89
XX
XX RESULT 6
XX AAB01905
XX AAB01905;
XX 18-SEP-2000 (first entry)
XX
XX Human plasminogen kringle 1-4 (angiotensin).
XX
XX Plasminogen; human; kringle domain; endothelial cell proliferation;
XX angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
XX antiproliferative; antiinflammatory; antitumor; antineoplastic; antiarthritic;
XX antiangiogenic; cancer; tumour; autoimmune disease.
XX
XX Homo sapiens.
XX

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XX US6057122-A.
PD 02-MAY-2000.
XX PF
XX 05-MAY-1997; 97US-0851350.
PR 03-MAY-1996; 96US-0643219.
PR 03-APR-1997; 97US-0832087.
PA (ABBO) ABBOTT LAB.
XX Davison DJ;
XX WPI: 2000-349573/30.
XX
XX Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer,
PT involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
PT Example 17; Page -, 48pp; English.

PS The invention relates to a method of preparing plasminogen kringles 5 CC and peptide fragments. The method comprises mixing mammalian plasminogen CC and elastase in the ratio 1:100-1:300, followed by incubating and isolating CC the fragment. The kringle 5 peptides are inhibitors of angiotensin and CC endothelial cell proliferation and migration. The peptides are useful CC for treating angiogenic diseases, primary and metastatic solid tumours CC and carcinomas of various organs such as breast, genital tract, CC endocrine glands, skin, tumours of the brain and eyes and solid tumours CC arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune CC diseases (e.g., Rheumatoid arthritis), ocular diseases, skin diseases CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber Syndrome), diseases caused by excessive or abnormal stimulation of CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch CC disease and ulcers). The peptides are also useful as a birth control CC agent which inhibits ovulation and establishment of the placenta. CC Sequences AAB01906-8019 represent fragments of human plasminogen used in an exemplification of the invention.
CC Note: This sequence is not shown in the specification, but is derived from the full length human plasminogen sequence (AAB01887) shown in figure 1.
CC SQ Sequence 364 AA;

SQ Query Match 84.9%; Score 444; DB 21; Length 364;
Best Local Similarity 82.0%; Pred. No. 2.8e-37;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0

OY 1 VROCYNHGSGSYRGFTTITVTGRTCSWSMTPHRHQTPEPNYPNDGLTMNYCRNPADT 60
DB :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
276 VQDCVHGGCGGYRGSTTTTGKKCKQSMSMTPHRHQTPEPNYPNAGLTMYVCRRPADK 335
OY 61 GPWCFTTPDIRWEYCNIILTRCSDTEIGTV 89
DB :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
336 GPWCFTTPDIRWEYCNIILKSCSDEASIV 364

RESULT 7
AAVS3868
ID AAVS3868 standard; protein, 369 AA.
XX AAVS3868;
XX AC
DT 13-MAR-2000 (first entry)
XX
DE Amino acid sequence of human angiotensin protein.
KW Human; plasminogen; angiotensin; greenstafin; chromolytic factor;
KW angiogenesis inhibitory protein; proliferation; angiogenesis; cancer;
KW vascular endothelial cell; ophthalmic disease; glaucoma;

KW diabetic retinopathy; arthritis; psoriasis.
XX
OS Homo sapiens.
XX
PN MO9961464-A1.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-KR0263.
XX
PR 28-MAY-1998; 98KR-0019535.
XX 27-MAY-1999; 99KR-0019144.
XX
PA (GREC) KOREA GREEN CROSS CORP.
XX
PI You WK, So SH, Ahn BC, Lee H, Jung S, Kim Y, Lee JH, Hong Y;
PI Joe YA, Chang S;
XX
DR WPI; 2000-086703/07.
XX
PT Purifying angiogenesis inhibitors produced as recombinant proteins in
PT Escherichia coli, useful as anticancer agents and for treating ocular
PT diseases -
XX
PS Claim 2; Page 45-47; 55pp; English.
XX
CC The present sequence represents the human angiostatin protein. It
CC is derived from the plasminogen protein, and comprises amino acids
CC 99-467. Greenstatin is also derived from plasminogen, and comprises
CC amino acids 101-354. Angiostatin and greenstatin are used as
CC thrombolytic factors and angiogenesis inhibitory proteins. Angiostatin
CC contains the kringle 1-4 region of plasminogen, and greenstatin contains
CC the kringle 1-3 region of plasminogen. As both proteins contain a high
CC number of disulphide bonds, they are difficult to purify. The
CC specification describes a method for the purification of such
CC angiogenesis inhibitory proteins. The method comprises solubilising
CC the proteins, produced as inclusion bodies in Escherichia coli and
CC refolding the solubilised fraction in buffer containing urea and
CC glutathione. The angiogenesis inhibitory proteins specifically inhibit
CC proliferation of vascular endothelial cells, but not that of
CC non-endothelial cancers or normal cells. The angiogenesis inhibitory
CC proteins are used to suppress angiogenesis, specifically for treating
CC cancers (e.g. of lung, skin and brain) or ophthalmic diseases (e.g.
CC glioma and diabetic retinopathy), but also arthritis and psoriasis.
XX
SQ Sequence 369 AA;
XX
Query Match 84.9%; Score 444; DB 21; Length 369;
Best Local Similarity 82.0%; Pred. No. 2.8e-37;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
XX
QY 1 VROCHNGNGOSYRGFTSTVTGTCQSSMTPHRQRTPEPNYDGLTMNCRPADDT 60
DB 276 VDDCYHGDQSGYRGFTSTVTGTCQSSMTPHRQRTPEPNYDGLTMNCRPADDK 335
XX
QY 61 GPMCFITDPSIRWEXCNLTRCSDEGTGVV 89
DB 336 GPMCFITDPSIRWEXCNLTRCSDEGTGVV 364
XX
RESULT 8
AAV79226
ID AAV79226 standard; Protein; 374 AA.
XX
AC AAV79226;
XX
DT 19-JUN-2000 (First entry)
XX
DE Angiogenesis inhibitor obtained by plasminogen cleavage.
XX
KW Angiogenesis inhibitor; plasminogen; human; K4 protease;
KW snake venom; cobra; antimetastatic; cytosolic; antitumour; tumour;
KW prostate cancer; breast cancer; colon cancer; lung cancer;
XX

KW leukaemia; metastasis; contraceptive; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 264
FT /note- "N-glycosylated"
XX
PN WO200010506-A2.
XX
PD 02-MAR-2000.
XX
PF 19-AUG-1999; 99WO-US18877.
XX
PR 20-AUG-1998; 98US-0097244.
XX
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX
PI Mann KG, Jenny NS;
XX
DR WPI; 2000-246485/21.
XX
PT New angiogenesis inhibitors useful for treating solid tumors,
PT leukemias, tumor metastasis, benign tumor, rheumatoid arthritis,
PT psoriasis and ocular angiogenic diseases -
XX
PS Claim 1; Fig 10; 72pp; English.
XX
CC The present sequence represents a preferred angiogenesis inhibitor
CC of the invention that is obtained by cleavage of human plasminogen
CC with splitting cobra (Naja nigricollis nigricollis) venom K4
CC protease and plasmin. The K4 protease cleaves native plasminogen
CC following amino acid residue 452, with little or no disruption of
CC the first 4 plasminogen kringles. Plasmin cleaves between residues
CC 77 and 78 of human plasminogen. Thus, the present protein spans
CC amino acid residues 78-451 of plasminogen. The angiogenesis
CC inhibitors obtained from plasminogen can be used to inhibit tumour
CC growth in a mammal, preferably human. They are useful for treating
CC angiogenesis-associated diseases such as: solid tumours, prostate
CC cancer, breast cancer, colon cancer and lung cancer (claimed);
CC blood-borne tumors such as leukaemia; metastasis; benign tumours;
CC rheumatoid arthritis; psoriasis; ocular angiogenic diseases;
CC myocardial angiogenesis; plaque neovascularization; telangiectasia;
CC haemophilic joints; angiodioma; wound granulation; excessive or
CC abnormal stimulation of endothelial cells; and as birth control
CC agents by preventing vascularization required for embryo
CC implantation. The inhibitors are administered also to extend the
CC durability of micrometastases and to stabilize any residual primary
CC tumour.
XX
SQ Sequence 374 AA;
XX
Query Match 84.9%; Score 444; DB 21; Length 374;
Best Local Similarity 82.0%; Pred. No. 2.9e-37;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
XX
QY 1 VROCHNGNGOSYRGFTSTVTGTCQSSMTPHRQRTPEPNYDGLTMNCRPADDT 60
DB 277 VDDCYHGDQSGYRGFTSTVTGTCQSSMTPHRQRTPEPNYDGLTMNCRPADDK 336
XX
QY 61 GPMCFITDPSIRWEXCNLTRCSDEGTGVV 89
DB 337 GPMCFITDPSIRWEXCNLTRCSDEGTGVV 365
XX
RESULT 9
AAV79225
ID AAV79225 standard; Protein; 375 AA.
XX
AC AAV79225;
XX
DT 19-JUN-2000 (First entry)
XX

DE Angiogenesis inhibitor obtained by plasminogen cleavage.
 XX
 XX Angiogenesis inhibitor; plasminogen; human; K4 protease;
 KW snake venom; cobra; antimetastatic; cytosolic; antitumor; tumour;
 KW prostate cancer; breast cancer; colon cancer; lung cancer;
 KW leukemia; metastasis; contraceptive; therapy.
 XX
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 265
 FT /note- "N-glycosylated"
 XX
 XX MO200010506-A2.
 PN
 PD 02-MAR-2000.
 XX
 XX 19-AUG-1999; 99MO-US18877.
 PF
 XX 20-AUG-1998; 98US-0097244.
 PR
 XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 PA
 PI Mann KG, Jenny NS;
 PI WPI; 2000-246485/21.
 DR
 XX New angiogenesis inhibitors useful for treating solid tumors,
 PT leukemias, tumor metastasis, benign tumor, rheumatoid arthritis,
 PT prolatias and ocular angiogenic diseases
 XX
 XX Claim 1; Fig 9; 72pp; English.
 PS
 XX The present sequence represents a preferred angiogenesis inhibitor
 CC of the invention that is obtained by cleavage of human plasminogen
 CC with splitting cobra (Naja nigricollis nigricollis) venom K4
 CC protease and plasmin. The K4 protease cleaves native plasminogen
 CC following amino acid residue 452, with little or no disruption of
 CC the first 4 plasminogen kringles. Plasmin cleaves between residues
 CC 77 and 78 of human plasminogen. Thus, the present protein spans
 CC amino acid residues 77-451 of plasminogen. The angiogenesis
 CC inhibitors obtained from plasminogen can be used to inhibit tumor
 CC growth in a mammal, preferably human. They are useful for treating
 CC angiogenesis-associated diseases such as: solid tumors, prostate
 CC cancer, breast cancer, colon cancer and lung cancer (claimed);
 CC blood-borne tumors such as leukemia; metastasis; benign tumors;
 CC rheumatoid arthritis; psoriasis; ocular angiogenic diseases;
 CC myocardial angiogenesis; plaque neovascularization; telangiectasis;
 CC hemophilic joints; angiofibroma; wound granulation; excessive or
 CC abnormal stimulation of endothelial cells; and as birth control
 CC agents by preventing vascularization required for embryo
 CC implantation. The inhibitors are administered also to extend the
 CC dormancy of micrometastases and to stabilize any residual primary
 CC tumour.
 CC
 XX
 SQ Sequence 375 AA;
 Query Match 84.9%; Score 444; DB 21; Length 375;
 Best Local Similarity 82.0%; Pred. No. 2.9e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 VROCYHNGSGSYRGTFSTVYTGRTCSQSSMTPHRHQRTPEYNYNDGLTMYNCRNPADT 60
 DB 278 VQDCTHGDGOSYRGTSSTTTTGKCCQSSMTPHRHQRTPEYNYNDGLTMYNCRNPADK 337
 QY 61 GPMCFITDPSIRMEYCNLTRCSPTDEGTIV 89
 DB 338 GPMCFITDPSIRMEYCNLTRCSPTDEASIV 366
 RESULT 10
 ID AAM07579 standard; protein; 378 AA.

XX
 XX AAM07579;
 AC
 XX 22-JUN-1997 (first entry)
 DT
 XX Human kringles 1-4BKLS.
 DE
 XX
 XX angiotatin; plasminogen; kringles; angiogenesis; cancer; arthritis;
 KW macular degeneration; diabetic retinopathy.
 XX
 XX Homo sapiens.
 OS
 FH Homo sapiens.
 FT MO9635774-A2.
 FT 14-NOV-1996.
 XX
 XX 26-APR-1996; 96MO-US05856.
 PF
 XX 08-MAR-1996; 96US-0612788.
 PR 26-APR-1995; 95US-0429743.
 PR 22-FEB-1996; 96US-0605598.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA
 PI Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;
 PI WPI; 1996-518662/51.
 DR
 XX Use of angiotatin fragments or aggregates - for inhibiting
 PT endothelial cell proliferation and treating angiogenesis-mediated
 PT diseases, e.g. cancer, arthritis or diabetic retinopathy
 XX
 XX Claim 4; Page 140-141; 203pp; English.
 PS
 XX The invention relates to new methods and compositions for
 CC inhibiting endothelial cell proliferation, using as active component
 CC an angiotatin fragment, a combination of angiotatin fragments, or
 CC aggregate angiotatin. The fragment is preferably derived from murine,
 CC human, Rhesus, porcine or bovine plasminogen and is a kringles 1,
 CC kringles 2, kringles 3, kringles 2-3, kringles 1-3, kringles 1-2, kringles
 CC 1-4 or kringles 1-4BKLS protein. The aggregate angiotatin has a Mol. wt.
 CC of 45-65 kD and is derived from a plasminogen fragment beginning at
 CC approximately amino acid number 98 of murine, human, Rhesus, porcine or
 CC bovine plasminogen. The active component can be used for treating
 CC angiogenesis-mediated diseases such as cancer, arthritis, macular
 CC degeneration and diabetic retinopathy. It can also be used to develop
 CC antibodies for use in diagnosis, detection and therapy.
 CC The present sequence, human kringles 1-4BKLS, is a specific angiotatin
 CC fragment which can be used in the invention.
 CC
 XX
 SQ Sequence 378 AA;
 Query Match 84.9%; Score 444; DB 17; Length 378;
 Best Local Similarity 82.0%; Pred. No. 2.9e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 VROCYHNGSGSYRGTFSTVYTGRTCSQSSMTPHRHQRTPEYNYNDGLTMYNCRNPADT 60
 DB 282 VQDCTHGDGOSYRGTSSTTTTGKCCQSSMTPHRHQRTPEYNYNDGLTMYNCRNPADK 341
 QY 61 GPMCFITDPSIRMEYCNLTRCSPTDEGTIV 89
 DB 342 GPMCFITDPSIRMEYCNLTRCSPTDEASIV 370
 RESULT 11
 ID AAB16450 standard; protein; 378 AA.
 AC AAB16450;
 XX
 XX 27-OCT-2000 (first entry)
 DT
 XX

DE Human angiotensin protein sequence.

XX Angiogenesis-inhibiting protein receptor; angiogenesis; angiotensin;
 XX endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;
 KW psoriasis; scleroderma; myocardial angiotensin; Crohn's disease;
 KW cerebral collateral; arteriovenous malformation; rubecosis; cancer;
 KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;
 KW Helicobacter related disease; fracture; cat scratch fever.

XX Homo sapiens.

PN WO200032631-A2.

PD 08-JUN-2000.

PF 06-DEC-1999; 99MO-US28897.

XX 04-DEC-1998; 98US-0206059.

XX (ENTR-) ENTREMED INC.

PI Macdonald NJ, Sim KL;

XX WPI; 2000-412290/35.

XX New angiogenesis-inhibiting protein receptors, useful in methods for
 PT treating diseases and processes that are mediated by angiogenesis, such
 PT as solid tumours, psoriasis, scleroderma and myocardial angiogenesis -
 PS Disclosure; Figure 2; 100pp; English.

XX This invention relates to angiogenesis-inhibiting protein receptors, and
 CC the DNA sequences encoding them. Angiogenesis is the generation of new
 CC blood vessels into a tissue, and normally occurs in wound healing,
 CC foetal and embryonal development and the formation of the corpus luteum,
 CC endometrium and placenta. Angiotensin is a protein (see AAB16450 and
 CC AAB68202) involved in angiogenesis, and has an amino acid sequence
 CC similar to that of a plasminogen fragment (see murine plasminogen
 CC AAB16490). Angiotensin has the ability to inhibit angiogenesis.
 CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and
 CC AAB68203). Sequences AAB68242 and AAB16522 represent coding and protein
 CC sequences of human laminin. Laminin is an angiotensin binding and protein,
 CC and some of the peptides of the invention share homology with regions of
 CC laminin. Peptides AAB16452-16521 (excluding AAB16490) are the
 CC angiotensin-inhibiting protein receptor fragments of the invention. The
 CC peptides bind either angiotensin or endostatin and can be used in methods
 CC for treating diseases and processes that are mediated by angiogenesis,
 CC such as solid tumours, psoriasis, scleroderma, myocardial angiotensin,
 CC Crohn's disease, cerebral collaterals, arteriovenous malformations,
 CC rubecosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,
 CC Helicobacter related diseases, fractures, placenta and cat scratch
 CC fever. They are useful for the detection and prognosis of cancer. DNA
 CC sequences A628204-A628241 encode the peptides of the invention.

XX Sequence 378 AA;

XX SQ

Query Match 84.9%; Score 444; DB 21; Length 378;
 Best Local Similarity 82.0%; Pred. No. 2.9e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 1 VROCCHNGGSGYRGFTSTTVTGRTCCQSSMTPHRHQRTPENYPNDGLTMNYCRNPDA DT 60
 Db 282 VQDCYHGGGQSYRGFTSTTVTGRTCCQSSMTPHRHQRTPENYPNDGLTMNYCRNPDA DX 341
 282 VQDCYHGGGQSYRGFTSTTVTGRTCCQSSMTPHRHQRTPENYPNDGLTMNYCRNPDA DX 341

OY 61 GPMCFITDPSIRWEYCNLTRCSPTDGTGV 89
 Db 342 GPMCFITDPSIRWEYCNLTRCSPTDGTGV 370

RESULT 12
 AAM48894 standard; Protein; 378 AA.

AC AAM48894;

XX 04-APR-2002 (first entry)

XX Human angiotensin protein.

DE Human angiotensin protein.

XX Human; angiotensin; endostatin; angiogenesis; cancer; metastasis;
 KW psoriasis; scleroderma; Crohn's disease; corneal disease;
 KW retinopathy; arthritis; wound healing; Helicobacter pylori; peptic ulcer;
 KW gene therapy; angiotensin antagonist; endostatin antagonist;
 KW antiangiogenic; cytosolic; antiarthritic; antiinflammatory;
 KW cerebroprotective; antidiabetic; virucide; antipyretic; vulnerary;
 KW gynaecological; cat scratch fever.

XX Homo sapiens.

XX WO200193897-A2.

XX 13-DEC-2001.

XX 04-JUN-2001; 2001MO-US17947.

XX 02-JUN-2000; 2000US-209065P.

XX 08-MAY-2001; 2001US-289387P.

XX (ENTR-) ENTREMED INC.

PI Sim KL, Macdonald NJ;

XX WPI; 2002-130569/17.

XX Regulating angiogenesis and treatment of angiogenesis-mediated
 PT diseases, e.g. hemangioma, tumors or cancer, by administering a
 PT tropomyosin binding compound or actin disrupting compound -
 PS Disclosure; Fig 2; 95pp; English.

XX The present invention relates to methods of regulating angiogenesis in an
 CC individual by administering an angiogenesis regulating composition
 CC comprising a tropomyosin binding compound or an actin disrupting
 CC compound. The compositions are useful for treating diseases and processes
 CC mediated by angiogenesis including haemangioma, solid tumours, blood
 CC borne tumours, leukaemia, metastasis, Crohn's disease, coronary or
 CC cerebral collaterals, arthritis, diabetic neovascularisation, macular
 CC degeneration, wound healing, Helicobacter related diseases, ovulation,
 CC menstruation, and cat scratch fever. The present sequence is a protein,
 CC described in the exemplification of the invention.

XX Sequence 378 AA;

XX SQ

Query Match 84.9%; Score 444; DB 23; Length 378;
 Best Local Similarity 82.0%; Pred. No. 2.9e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 1 VROCCHNGGSGYRGFTSTTVTGRTCCQSSMTPHRHQRTPENYPNDGLTMNYCRNPDA DT 60
 Db 282 VQDCYHGGGQSYRGFTSTTVTGRTCCQSSMTPHRHQRTPENYPNDGLTMNYCRNPDA DX 341
 282 VQDCYHGGGQSYRGFTSTTVTGRTCCQSSMTPHRHQRTPENYPNDGLTMNYCRNPDA DX 341

OY 61 GPMCFITDPSIRWEYCNLTRCSPTDGTGV 89
 Db 342 GPMCFITDPSIRWEYCNLTRCSPTDGTGV 370

RESULT 13
 AA02105 standard; Protein; 380 AA.

XX AA02105;

XX 16-JUL-1999 (first entry)

XX A multifunctional protein of the invention.

KM Angiotensin; endostatin; interferon; thrombospondin;
 KM interferon-inducible protein; platelet factor 4; anti-angiogenic;
 KM anti-tumor; multifunctional protein; angiogenic-mediated disease;
 KM cancer; diabetic retinopathy; macular degeneration; arthritis;
 KM tumor cell production.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN MO9916889-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 30-SEP-1998; 98WC-US20464.
 XX
 PR 01-OCT-1997; 97US-0060609.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 PI Bolanowski MA, Caparon MH, Casperson GF, Gregory SA;
 PI Klein BK, McKearn JP;
 DR WPI; 1999-255098/21.
 XX
 PT New multifunctional proteins useful for treating angiogenic-mediated
 PT diseases
 XX
 PS Claim 5; Page 100-101; 121pp; English.
 XX
 CC The specification describes multifunctional proteins which comprise
 CC combinations of angiotensin, endostatin, interferon, thrombospondin,
 CC interferon-inducible protein and platelet factor 4, and have
 CC anti-angiogenic and/or anti-tumor activity. The multifunctional protein
 CC may exhibit useful properties such as having similar or greater
 CC biological activity when compared to a single factor or by having
 CC improved half-life or decreased adverse side effects, or a combination
 CC of these properties. The proteins can be used for treating an
 CC angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular
 CC degeneration, or arthritis. They can also be used for inhibiting the
 CC production of tumor cells (characteristic of lung, breast, ovarian,
 CC prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma,
 CC hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor
 CC growth. The present sequence represents a multifunctional protein of the
 CC invention.
 CC
 XX
 SQ Sequence 380 AA;
 XX
 Query Match 84.9%; Score 444; DB 20; Length 380;
 Best Local Similarity 82.0%; Pred. No. 2.9e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 VROCYNHGQSYRGTESTVTYGRTCQSWSSMTPHRHQRTPEYNDGLTMNYCRNPADT 60
 Db 284 VQDCYHGDGQSYRGSTSTTTGKKCQSWSSMTPHRHQRTPEYNDGLTMNYCRNPADK 343
 QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTIV 89
 Db 344 GPMCFITDPSIRWEYCNLTRCSDTEASIV 372
 XX
 RESULT 14
 AAW51457
 ID AAW51457 standard; protein: 437 AA.
 XX
 AC AAW51457;
 XX
 DT 02-SEP-1998 (first entry)
 XX
 DE Human plasminogen fragment with neovascularisation inhibiting activity.
 XX
 KM Human plasminogen; neovascularisation; angiotensin; inhibition;
 KM elastase; Sepharose.
 XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 4..81
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 25..64
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 53..76
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 108..187
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 129..170
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 158..182
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 194..313
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 204..212
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 234..250
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 326..393
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 356..372
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 383..411
 FT Disulfide-bond /label= Disulphide_bond
 XX
 PN JP10158300-A.
 XX
 PD 16-JUN-1998.
 XX
 PF 28-NOV-1996; 96GP-0317250.
 XX
 PR 28-NOV-1996; 96GP-0317250.
 XX
 PA (SUZUKI) SUZUKI KK.
 XX
 DR WPI; 1998-393476/34.
 XX
 PT Human plasminogen derived polypeptide - has neovascularisation
 PT inhibiting activity
 XX
 PS Claim 1; Page 2; 16pp; Japanese.
 XX
 CC The invention relates to a neovascularisation inhibitor which comprises
 CC amino acids 355-791 of human plasminogen. Also claimed are a method for
 CC the preparation of angiotensin, and angiotensin prepared by this method.
 CC The human plasminogen protein fragment is prepared by: (a) applying human
 CC plasminogen to a lysine Sepharose column to separate it into plasminogen
 CC form 1 and form 2; (b) separating plasminogen form 1 and form 2 and
 CC digesting them with elastase; (c) fractionating the elastase-decomposed
 CC product of form 1 plasminogen and form 2 plasminogen in a lysine
 CC Sepharose column; (d) collecting the fractions bound to the lysine
 CC an Aminohexyl Sepharose column; and (f) collecting the fraction bound to
 CC the Aminohexyl Sepharose column. This human plasminogen fragment can be
 CC used to inhibit growth of vascular endothelial cells. The present
 CC sequence represents amino acids 355-791 of human plasminogen.
 CC
 XX
 SQ Sequence 437 AA;
 XX
 Query Match 84.9%; Score 444; DB 19; Length 437;
 Best Local Similarity 82.0%; Pred. No. 3.4e-37;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 VROCYNHGQSYRGTESTVTYGRTCQSWSSMTPHRHQRTPEYNDGLTMNYCRNPADT 60
 Db 1 VQDCYHGDGQSYRGSTSTTTGKKCQSWSSMTPHRHQRTPEYNDGLTMNYCRNPADK 60
 QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTIV 89
 Db 61 GPMCFITDPSIRWEYCNLTRCSDTEASIV 89

RESULT 15

AY79224 standard; Protein; 452 AA.

AC MAY79224;

DT 19-JUN-2000 (first entry)

Angiogenesis inhibitor obtained by human plasminogen cleavage.

K4 Angiogenesis inhibitor; plasminogen; human; K4 protease;

KW cytostatic; antitumour; tumour; prostate cancer; breast cancer

therapy.

Homo sapiens.

| EM | Key | Location/Qualifiers |
|----|-----|---------------------|
| FH | 1 | 57 |

```
FT      /notes= "terminal activation peptide"
EM      57 50
```

FT /note= "plasmin cleavage site"

| FT | /label= Gln, Glu |
|-------------|------------------|
| W: 2.550000 | 2.43 |

```

E7      /label= Gln, Glu
E8      /label= Gln, Glu
E9      /label= Gln, Glu

```

| PT | Modified date | /note= "residue may be absent" |
|----|---------------|--------------------------------|
| EM | 2008 | |

| EM | FT | Modified site | /note- "N-glycosylated" |
|-----|----|---------------|-------------------------|
| 345 | | | |

/note- "N-glycosylated
yy

PN WO200010506-A2
yy

PD 02-MAR-2000
YY

PE 19-AUG-1999; 99MO-US18877.
XY

PR 20-AUG-1998; 98US-0097244.
XX

PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE
YY

PI Mann KG, Jenny NS;
YY

DR WPI; 2000-246485/21.

PT New angiogenesis inhibitors useful for treating solid tumors,
PT leukemias, tumor metastasis, benign tumor, rheumatoid arthritis,
PT psoriasis and ocular angiogenic diseases -

PS Claim 14; Fig 8; 72pp; English.

The present sequence represents an angiogenesis inhibitor obtained by cleavage of human plasminogen with snake venom K4 protease from spitting cobra (*Naja nigricollis nigricollis*). The K4 protease cleaves the plasminogen following amino acid residue 432, producing an angiogenesis inhibitor with little or no disruption of the first 4 plasminogen kringles. Further, preferred angiogenesis inhibitors of the invention are obtained by plasmin cleavage of this K4 protease-cleaved plasminogen fragment (see AA779225 and AA779226). The angiogenesis inhibitors are used for inhibiting tumour growth in a mammal, preferably human. They are useful for treating angiogenesis-associated diseases such as: solid tumours, prostate cancer, breast cancer, colon cancer and lung cancer (claimed); blood-borne tumours such as leukaemia, metastasis; benign tumours; rheumatoid arthritis; psoriasis; ocular angiogenic diseases; myocardial angiogenesis; plaque neovascularization; telangiectasia; haemophilic joints; angiodiroma; wound granulation; excessive or abnormal stimulation of endothelial cells; and as birth control

CC agents by preventing vascularization required for embryo
CC implantation. The inhibitors are administered also to extend the
CC dormancy of micrometastases and to stabilize any residual primary
CC tumour.

SQ Sequence 452 AA;

| | | | | |
|-------------|--------|------------|--------|-------------|
| Query Match | 84.98; | Score 444; | DB 21; | Length 452; |
|-------------|--------|------------|--------|-------------|

Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

1 VROC YHNGSGSYRGTFSTVTGRTCSWSSMTPHRHQRTPENYPNDGLTMYCRNPBBDT 600

Db 355 VQDCYHGDGQSYRGTSTTTTGKCCQSWSMTPHRHQKTPEPNAGLTMTYCRNPDAKD 414

61 GPWCFTTDPISIRWXCNI TRCSDTEGTVV

Db 415 GPMCFITDPSVRWEXCNLKKCSGTEASV 443

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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:24:03 ; Search time 26.0977 Seconds
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Maximum Match 100%
Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------------|-------------------|
| 1 | 517 | 98.9 | 1169 | US-09-870-759-126 | Sequence 126, App |
| 2 | 517 | 98.9 | 1169 | US-09-751-708A-126 | Sequence 126, App |
| 3 | 447 | 85.5 | 368 | US-09-761-120-42 | Sequence 42, Appl |
| 4 | 447 | 85.5 | 368 | US-10-402-364-42 | Sequence 42, Appl |
| 5 | 444 | 84.9 | 378 | US-09-873-676-1 | Sequence 1, Appl |
| 6 | 444 | 84.9 | 378 | US-09-335-325-42 | Sequence 42, Appl |
| 7 | 444 | 84.9 | 378 | US-10-131-241-42 | Sequence 42, Appl |
| 8 | 444 | 84.9 | 391 | US-10-304-287-7 | Sequence 7, Appl |
| 9 | 444 | 84.9 | 394 | US-10-304-287-8 | Sequence 8, Appl |
| 10 | 444 | 84.9 | 458 | US-09-946-893-4 | Sequence 4, Appl |
| 11 | 444 | 84.9 | 569 | US-09-946-893-5 | Sequence 5, Appl |
| 12 | 444 | 84.9 | 571 | US-09-946-893-8 | Sequence 8, Appl |
| 13 | 444 | 84.9 | 576 | US-09-946-893-6 | Sequence 6, Appl |
| 14 | 444 | 84.9 | 791 | US-09-967-386-1 | Sequence 1, Appl |
| 15 | 444 | 84.9 | 791 | US-10-304-287-1 | Sequence 1, Appl |

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| 16 | 444 | 84.9 | 810 | US-09-946-893-2 | Sequence 2, Appl |
| 17 | 444 | 84.9 | 810 | US-10-237-144-1 | Sequence 1, Appl |
| 18 | 444 | 84.9 | 810 | US-10-193-656-2 | Sequence 2, Appl |
| 19 | 435 | 83.2 | 363 | US-10-292-418-11 | Sequence 11, Appl |
| 20 | 422 | 80.7 | 352 | US-09-761-120-40 | Sequence 40, Appl |
| 21 | 422 | 80.7 | 352 | US-09-335-325-40 | Sequence 40, Appl |
| 22 | 422 | 80.7 | 352 | US-10-402-364-40 | Sequence 40, Appl |
| 23 | 422 | 80.7 | 352 | US-10-131-241-40 | Sequence 40, Appl |
| 24 | 417 | 79.7 | 78 | US-09-753-064-5 | Sequence 5, Appl |
| 25 | 417 | 79.7 | 78 | US-09-761-120-23 | Sequence 23, Appl |
| 26 | 417 | 79.7 | 78 | US-09-335-325-23 | Sequence 23, Appl |
| 27 | 417 | 79.7 | 78 | US-10-267-137-9 | Sequence 9, Appl |
| 28 | 417 | 79.7 | 78 | US-10-402-364-23 | Sequence 23, Appl |
| 29 | 417 | 79.7 | 78 | US-10-402-364-41 | Sequence 41, Appl |
| 30 | 417 | 79.7 | 78 | US-10-131-241-23 | Sequence 23, Appl |
| 31 | 413 | 79.0 | 451 | US-10-157-369-2 | Sequence 2, Appl |
| 32 | 412 | 78.8 | 364 | US-10-157-369-4 | Sequence 4, Appl |
| 33 | 404 | 77.2 | 359 | US-10-292-418-40 | Sequence 40, Appl |
| 34 | 400 | 76.5 | 378 | US-09-761-120-41 | Sequence 41, Appl |
| 35 | 400 | 76.5 | 378 | US-09-335-325-41 | Sequence 41, Appl |
| 36 | 400 | 76.5 | 378 | US-10-402-364-41 | Sequence 41, Appl |
| 37 | 400 | 76.5 | 378 | US-10-131-241-41 | Sequence 41, Appl |
| 38 | 400 | 76.5 | 459 | US-09-761-120-46 | Sequence 46, Appl |
| 39 | 400 | 76.5 | 459 | US-10-402-364-46 | Sequence 46, Appl |
| 40 | 400 | 76.5 | 812 | US-09-788-142-1 | Sequence 1, Appl |
| 41 | 400 | 76.5 | 812 | US-09-761-120-1 | Sequence 1, Appl |
| 42 | 400 | 76.5 | 812 | US-09-873-676-81 | Sequence 81, Appl |
| 43 | 400 | 76.5 | 812 | US-09-335-325-1 | Sequence 1, Appl |
| 44 | 400 | 76.5 | 812 | US-10-402-364-1 | Sequence 1, Appl |
| 45 | 400 | 76.5 | 812 | US-10-131-241-1 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1
US-09-870-759-126
; Sequence 126, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-126

Query Match 98.9%; Score 517; DB 10; Length 1169;
Best Local Similarity 98.9%; Pred. No. 9e+49; 1; Indels 0; Gaps 0;
Matches 88; Conservative 0; Mismatches 1;

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| QY | 1 | VRQCHNGGQSYRGFTSTTVGRTGQSSMTPHRHQRTPENYNDGLTNNYCRNPADT 60 |
| DB | 742 | VRQCHNGGQSYRGFTSTTVGRTGQSSMTPHRHQRTPENYNDGLTNNYCRNPADT 801 |
| QY | 61 | GPWCFTDPSIRWEYCNLTRCSDEGTIV 89 |
| DB | 802 | GPWCFTDPSIRWEYCNLTRCSDEGTIV 830 |

RESULT 2
US-09-751-708A-126
; Sequence 126, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:

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:
: APPLICANT: TERMAN, David S
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
: FILE REFERENCE: 7511708
: CURRENT APPLICATION NUMBER: US/09/751,708A
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: US 60/173,371
: PRIOR FILING DATE: 1999-12-28
: NUMBER OF SEQ ID NOS: 166
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 126
: LENGTH: 1169
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-751-708A-126

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| Query Match | 98.9% | Score 517; | DB 12; | Length 1169; |
| Beat Local Similarity | 98.9% | Pred. No. 9e-49; | | |
| Matches | 88; | Conservative | 0; | Mismatches 1; Indels 0; Gaps 0 |
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| | | | | |
| DB | 742 | VROCYHGAGOSYRGFFSTTVTVGRGTCOSWSSMPHRRORTPEVYPNDGLTMYNCRAPDADT | 801 | |
| QY | 61 | GPWCFTTDPISIRMEYCNLTRCSDEGTGVV | 89 | |
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| DB | 802 | GPWCFTTMDPSIRMEYCNLTRCSDEGTGVV | 830 | |

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RESULT 3
US-09-761-120-42
Sequence 42, Application US/09761120
Patent No. US20020037847A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
TITLE OR INVENTION: Nucleic Acids Encoding Kring1e 1-5 Region Fragments of Plasminogen
FILE REFERENCE: 05940-0151 (43171-252068)
CURRENT FILING DATE: 2001-01-16
PRIORITY APPLICATION NUMBER: 09/309,821
PRIORITY FILING DATE: 1999-05-11
PRIORITY APPLICATION NUMBER: 08/866,735
PRIORITY FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.0
SEQ ID NO 42
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Kring1e 1-4 BKLS
US-09-761-120-42

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[illegible]

RESULT 4
US-10-402-364-42
; Sequence 42, Application US/10402364
; Publication No. US20040002459A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael

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APPLICANT: Folkman, M. Judah
TITLE OF INVENTION: Nucleic Acids Encoding Kringlike 1-5 Region Fragments of Plasminogen
FILE REFERENCE: 05213-2151 (43170-252068)
CURRENT APPLICATION NUMBER: US/10/402,364
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: US/09/761,120A
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 09/309,821
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 08/866,735
PRIOR FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Kringlike 1-4 BKLS
US-10-402-364-42

Query Match      85.5%; Score 447; DB 12; Length 368;
Best Local Similarity 82.0%; Pred. No. 1,5e-41;
Matches 73; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

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Db 272 VQDCYHGDGGSYRSTSTSTTTGKKCOASSMSTPHRHQRTPENYPRAGLTNNYCRPPADDK 331
QY 61 GPMCFCTTDPSTIRMEYCNLTRCSDEGIYV 89
Db 332 GPMCFCTTDPSTVRYMEYCNLTRCSDEASIV 360
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RESULT 5
US-09-873-676-1
/ Sequence 1, Application US/09873676
/ Patent No. US20020077289A1
/ GENERAL INFORMATION:
/ APPLICANT: MacDonald, Nicholas J.
/ APPLICANT: Sim, Kim L.
/ TITLE OF INVENTION: Angiotensin and Endostatin Binding Proteins and Methods of Use
/ FILE REFERENCE: 05213-0378 (43170-25933)
/ CURRENT APPLICATION NUMBER: US/09/873,676
/ PRIOR FILING DATE: 2001-06-04
/ PRIOR APPLICATION NUMBER: US 60/209,065
/ PRIOR FILING DATE: 2000-06-02
/ PRIOR APPLICATION NUMBER: US 60/289,387
/ PRIOR FILING DATE: 2001-05-08
/ NUMBER OF SEQ ID NOS: 123
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 378
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-873-676-1

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[illegible]

RESULT 6
US-09-335-325-42

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Sequence 42, Application US/09335325
Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
O'Reilly, Michael
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: KI-4BKLS
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-335-325-42
Query March 84.9%; Score 444; DB 10; Length 378;
Best Local Similarity 82.0%; Pred. No. 3.4e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 VRCCYHANGGOSYRGTFTTIVTGRTCSQSSWTPPHRQRTPEPNYDNDGILMNYCNPADAT 60
D 282 VQDCHYHDGGSYRSTSTTTTGKKCCQSSWTPPHRQKTPENYINAGILMNYCNPADK 341
QY 61 GPMCFCTTDPSTIRWEYCNLTTRCSDTEGTVV 89
D 342 GPMCFCTTDPSTIRWEYCNLTTRCSDTEASV 370
RESULT 7
US-10-131-241-42
Sequence 42, Application US/10131241
Publication No. US20030012792A1
GENERAL INFORMATION:
APPLICANT: Holtz, John W.
Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation

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; TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
; FILE REFERENCE: 05213-0344 43170-271565
; CURRENT APPLICATION NUMBER: US/10/131,241
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/413,049
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/086,586
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-241-42

Query Match      84.9%; Score 444; DB 15; Length 378;
Best Local Similarity 82.0%; Pred. No. 3.4e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Dy      1 VROCYNHGNGSYRGFTSTVTYTGRTCSQSWSMTPHRHQRPENYPNDGLTMNYCRNPDA DT 60
       |:|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      278 VPDCYHGDGGSYRGTSSTTTTGGKCKQSWSMTPHRHQRPENYPNAGLTMNYCRNPDA DK 337
       ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Oy      61 GPWCFTTDPESIRWEYCNLTRCSDTEGTIV 89
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      338 GPWCFTTDPESVRWEYCNLKKSCTEASVV 366
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 9
US-10-304-287-8
; Sequence 8, Application US/10304287
; Publication No. US20030083234A1
; GENERAL INFORMATION:
; APPLICANT: Walsman, David M.
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; APPLICANT: Kwon, MiJung
; FILE REFERENCE: ME02-001
; CURRENT APPLICATION NUMBER: US/10/304,287
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/333,866
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO 7
; LENGTH: 391
; TYPE: PRT
; ORGANISM: mammalian
US-10-304-287-7

Query Match      84.9%; Score 444; DB 15; Length 391;
Best Local Similarity 82.0%; Pred. No. 3.5e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Oy      1 VROCYNHGNGSYRGFTSTVTYTGRTCSQSWSMTPHRHQRPENYPNDGLTMNYCRNPDA DT 60
       |:|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      278 VPDCYHGDGGSYRGTSSTTTTGGKCKQSWSMTPHRHQRPENYPNAGLTMNYCRNPDA DK 337
       ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Oy      61 GPWCFTTDPESIRWEYCNLTRCSDTEGTIV 89
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      338 GPWCFTTDPESVRWEYCNLKKSCTEASVV 366
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 9
US-10-304-287-8
; Sequence 8, Application US/10304287
; Publication No. US20030083234A1
; GENERAL INFORMATION:
; APPLICANT: Walsman, David M.
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor

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FILE REFERENCE: ME02-001
CURRENT APPLICATION NUMBER: US/10/304,287
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US 60/333,866
PRIOR FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Word
SEQ ID NO 8
LENGTH: 394
TYPE: PRT
ORGANISM: mammalian
US-10-304-287-8

Query Match
Best Local Similarity 84.9%; Score 444; DB 15; Length 394;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRCCYHNGSGSYRGFTSTVTYGRCCQSWSMTPRHQRTPENYPNDGLTMNYCRNPADT 60
DB 278 VQDCYHGDGQSYRGFTSTVTYGRCCQSWSMTPRHQRTPENYPNAGLTMYNCRNPADK 337
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 89
DB 338 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 366

RESULT 10
US-09-946-893-4
Sequence 4, Application US/09946893
Patent No. US20020072494A1
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
FILE REFERENCE: Newburn
CURRENT APPLICATION NUMBER: US/09/946,893
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/230,893
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
US-09-946-893-4

Query Match
Best Local Similarity 84.9%; Score 444; DB 9; Length 458;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRCCYHNGSGSYRGFTSTVTYGRCCQSWSMTPRHQRTPENYPNDGLTMNYCRNPADT 60
DB 272 VQDCYHGDGQSYRGFTSTVTYGRCCQSWSMTPRHQRTPENYPNAGLTMYNCRNPADK 331
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 89
DB 332 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 360

RESULT 11
US-09-946-893-5
Sequence 5, Application US/09946893
Patent No. US20020072494A1
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
FILE REFERENCE: Newburn
CURRENT APPLICATION NUMBER: US/09/946,893
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/230,893
PRIOR FILING DATE: 2000-09-05
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NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 569
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
US-09-946-893-5

Query Match
Best Local Similarity 84.9%; Score 444; DB 9; Length 569;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRCCYHNGSGSYRGFTSTVTYGRCCQSWSMTPRHQRTPENYPNDGLTMNYCRNPADT 60
DB 374 VQDCYHGDGQSYRGFTSTVTYGRCCQSWSMTPRHQRTPENYPNAGLTMYNCRNPADK 433
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 89
DB 434 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 462

RESULT 12
US-09-946-893-8
Sequence 8, Application US/09946893
Patent No. US20020072494A1
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
FILE REFERENCE: Newburn
CURRENT APPLICATION NUMBER: US/09/946,893
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/230,893
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 571
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
US-09-946-893-8

Query Match
Best Local Similarity 84.9%; Score 444; DB 9; Length 571;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRCCYHNGSGSYRGFTSTVTYGRCCQSWSMTPRHQRTPENYPNDGLTMNYCRNPADT 60
DB 374 VQDCYHGDGQSYRGFTSTVTYGRCCQSWSMTPRHQRTPENYPNAGLTMYNCRNPADK 433
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 89
DB 434 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 462

RESULT 13
US-09-946-893-6
Sequence 6, Application US/09946893
Patent No. US20020072494A1
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
FILE REFERENCE: Newburn
CURRENT APPLICATION NUMBER: US/09/946,893
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/230,893
PRIOR FILING DATE: 2000-09-05
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NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 6
LENGTH: 576
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
US-09-946-893-6

Query Match 84.9%; Score 444; DB 9; Length 576;
Best Local Similarity 82.0%; Pred. No. 5.4e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRQCYHNGQSYRGTSYTTGRTQSWSMTPHRHQRTPEPNYNDGLTMNYCRNPADT 60
DB 374 VQDCYHGDQSYRGTSYTTGRTQSWSMTPHRHQRTPEPNYNDGLTMNYCRNPADK 433

QY 61 GPWCFTTDPISIRWEYCNLTRCSDTEGTV 89
DB 434 GPWCFTTDPISIRWEYCNLTRCSDTEASV 462

RESULT 14
US-09-967-386-1
Sequence 1, Application US/09967386
Patent No. US2002015992A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Henkin, Jack
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: ANTIANGIOGENIC POLYPEPTIDES AND METHODS
FILE REFERENCE: 6738-US-02
CURRENT APPLICATION NUMBER: US/09/967,386
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/236,550
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 791
TYPE: PRT
ORGANISM: Homo sapiens
US-09-967-386-1

Query Match 84.9%; Score 444; DB 10; Length 791;
Best Local Similarity 82.0%; Pred. No. 7.6e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRQCYHNGQSYRGTSYTTGRTQSWSMTPHRHQRTPEPNYNDGLTMNYCRNPADT 60
DB 355 VQDCYHGDQSYRGTSYTTGRTQSWSMTPHRHQRTPEPNYNDGLTMNYCRNPADK 414

QY 61 GPWCFTTDPISIRWEYCNLTRCSDTEGTV 89
DB 415 GPWCFTTDPISIRWEYCNLTRCSDTEASV 443

RESULT 15
US-10-304-287-1
Sequence 1, Application US/10304287
Publication No. US20030083234A1
GENERAL INFORMATION:
APPLICANT: Waleman, David M.
APPLICANT: Kwon, Mijung
TITLE OF INVENTION: Anti angiogenesis methods, compositions and uses therefor
FILE REFERENCE: ME02-001
CURRENT APPLICATION NUMBER: US/10/304,287
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US 60/333,866
PRIOR FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Word
SEQ ID NO 1
LENGTH: 791
TYPE: PRT
ORGANISM: mammalian
US-10-304-287-1

Query Match 84.9%; Score 444; DB 15; Length 791;
Best Local Similarity 82.0%; Pred. No. 7.6e-41;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRQCYHNGQSYRGTSYTTGRTQSWSMTPHRHQRTPEPNYNDGLTMNYCRNPADT 60
DB 355 VQDCYHGDQSYRGTSYTTGRTQSWSMTPHRHQRTPEPNYNDGLTMNYCRNPADK 414

QY 61 GPWCFTTDPISIRWEYCNLTRCSDTEGTV 89
DB 415 GPWCFTTDPISIRWEYCNLTRCSDTEASV 443

Search completed: January 12, 2004, 17:29:39
Job time : 26.0977 secs

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: angiogenesis inhibitor
NAME/KEY: MOD RES
LOCATION: (265)
OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-2

Query Match
Best Local Similarity 84.9%; Score 444; DB 4; Length 375;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Db 1 VROCYNHGSGSYRGFTSTVTGRTCSWSSMTPHRHQRTPEYVNDGLTMYCRNPADT 60
278 VQDCYHGDGSGYRGFTSTTTTGKCCSWSSMTPHRHQRTPEYVNDGLTMYCRNPADK 337

Qy 61 GPMCFITDPSIRWEYCNLTGCSPTGTVV 89
Db 338 GPMCFITDPSIRWEYCNLTGCSPTGTVV 366

RESULT 3
US-08-612-788-42
Sequence 42, Application US/08612788
Patent No. 5837682
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:

CLONE: K1-4BKLS
US-08-612-788-42

Query Match
Best Local Similarity 84.9%; Score 444; DB 2; Length 378;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VROCYNHGSGSYRGFTSTVTGRTCSWSSMTPHRHQRTPEYVNDGLTMYCRNPADT 60
Db 282 VQDCYHGDGSGYRGFTSTTTTGKCCSWSSMTPHRHQRTPEYVNDGLTMYCRNPADK 341

Qy 61 GPMCFITDPSIRWEYCNLTGCSPTGTVV 89
Db 342 GPMCFITDPSIRWEYCNLTGCSPTGTVV 370

RESULT 4
US-09-066-028-42
Sequence 42, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K1-4BKLS
US-09-066-028-42

Query Match
Best Local Similarity 84.9%; Score 444; DB 3; Length 378;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 89
DB 414 GPMCFITDPSIRWEYCNLTRCSDTEASVV 442

RESULT 8

US-09-377-250-4
Sequence 4, Application US/09377250
Patent No. 635364
GENERAL INFORMATION:
APPLICANT: MANN, KENNETH G.
APPLICANT: SMORDS JENNY, NANCY
TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
FILE REFERENCE: 48409/360
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 452
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: plasminogen fragment
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (53)
OTHER INFORMATION: Xaa = Gln or Glu
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (342)
OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-4

Query Match 84.9%; Score 444; DB 4; Length 452;
Best Local Similarity 82.0%; Pred. No. 2.2e-42;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VROCYHNGSGYRGFTSTVTGRTCCSSMTPHRHQRTPEYVNDGLTMNYCRNPADT 60
DB 355 VODCYHGDQSYRGSTSTTTTGKCCSSMTPHRHQRTPEYVNDGLTMNYCRNPADK 414
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 89
DB 415 GPMCFITDPSIRWEYCNLTRCSDTEASVV 443

RESULT 9

US-08-469-486-54
Sequence 54, Application US/08469486
Patent No. 573281
GENERAL INFORMATION:
APPLICANT: Thøgersen, Hans Christian
APPLICANT: Holte, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486

FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906

TELEX: 200154
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-486-54

Query Match 84.9%; Score 444; DB 1; Length 790;
Best Local Similarity 82.0%; Pred. No. 4.4e-42;
Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VROCYHNGSGYRGFTSTVTGRTCCSSMTPHRHQRTPEYVNDGLTMNYCRNPADT 60
DB 354 VODCYHGDQSYRGSTSTTTTGKCCSSMTPHRHQRTPEYVNDGLTMNYCRNPADK 413
QY 61 GPMCFITDPSIRWEYCNLTRCSDTEGTVV 89
DB 414 GPMCFITDPSIRWEYCNLTRCSDTEASVV 442

RESULT 10

US-08-469-658-54
Sequence 54, Application US/08469658
Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: Thøgersen, Hans Christian
APPLICANT: Holte, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070

REFERENCE/DOCKET NUMBER: 5940.US.PI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-938-3137
 TELEFAX: 847-938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 791 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE:
 DESCRIPTION: protein
 US-09-132-154-1

Query Match 84.9%; Score 444; DB 3; Length 791,
 Best Local Similarity 82.0%; Pred. No. 4.4e-42;
 Matches 73; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 VRQCYHNGSGSYRGFTSTVTGRTCSWSSMTPRHQRTPENYPNDGLTMNYCRNPADT 60
 DB 355 VQDCYHGDGOSYRGFTSTTTGKKCSWSSMTPRHQRTPENYPNAGLTMNYCRNPADK 414
 QY 61 GPWCFTTDPISIRNEYCNLTFCSDPTGTVV 89
 DB 415 GPWCFTTDPISIRNEYCNLTFCSDPTGTVV 443

Search completed: January 12, 2004, 17:27:15
 Job time: 12.7143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:19:12 : Search time 11.6391 Seconds
(without alignments)
710.580 Million cell updates/sec

Title: US-10-088-548-8

Perfect score: 508
Sequence: 1 EDDQMGNGKGYRGKATTV.....YTMNPKLFDYCDIPICASS 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 76:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 508 | 100.0 | 4548 | 1 S00657 | apoprotein(a) (EC |
| 2 | 432 | 85.0 | 810 | 2 B30848 | plasma (EC 3.4.21 |
| 3 | 430 | 84.6 | 810 | 1 PLHU | plasma (EC 3.4.21 |
| 4 | 416 | 81.9 | 460 | 2 B61545 | plasma (EC 3.4.21 |
| 5 | 415 | 81.7 | 455 | 2 A61545 | plasma (EC 3.4.21 |
| 6 | 409 | 80.5 | 790 | 1 PLRG | plasma (EC 3.4.21 |
| 7 | 406 | 79.9 | 812 | 1 PLMS | plasma (EC 3.4.21 |
| 8 | 406 | 79.9 | 812 | 1 PLBO | plasma (EC 3.4.21 |
| 9 | 388 | 76.4 | 810 | 2 I46260 | plasma (EC 3.4.21 |
| 10 | 243.5 | 47.9 | 169 | 2 A40522 | plasma (EC 3.4.21 |
| 11 | 243.5 | 47.9 | 716 | 1 JCS61 | macrophage-stimula |
| 12 | 242 | 47.6 | 123 | 2 C61545 | plasma (EC 3.4.21 |
| 13 | 241.5 | 47.5 | 711 | 1 A47136 | macrophage-stimula |
| 14 | 239.5 | 47.1 | 716 | 1 A40332 | macrophage-stimula |
| 15 | 239 | 47.0 | 2869 | 2 T18518 | apolipoprotein(a) |
| 16 | 237.5 | 46.8 | 710 | 1 I51283 | apolipoprotein(a) |
| 17 | 236 | 46.5 | 1420 | 2 A32869 | apolipoprotein(a) |
| 18 | 234.5 | 46.2 | 728 | 1 JH0579 | hepatocyte growth |
| 19 | 228 | 44.9 | 120 | 2 B61545 | plasma (EC 3.4.21 |
| 20 | 227.5 | 44.8 | 728 | 1 A35644 | hepatocyte growth |
| 21 | 227.5 | 44.8 | 728 | 1 A60185 | hepatocyte growth |
| 22 | 213 | 41.9 | 89 | 2 A60140 | plasma (EC 3.4.21 |
| 23 | 206.5 | 40.6 | 625 | 1 TBBO | chromin (EC 3.4.2 |
| 24 | 206 | 40.6 | 411 | 2 I51285 | hepatocyte growth |
| 25 | 199.5 | 39.3 | 336 | 2 S3879 | plasma precursor |
| 26 | 198.5 | 39.1 | 943 | 2 B45082 | neurotrophic recep |
| 27 | 195 | 38.4 | 617 | 2 S10511 | chromin (EC 3.4.2 |
| 28 | 191.5 | 37.7 | 622 | 1 TBHU | chromin (EC 3.4.2 |
| 29 | 187 | 36.8 | 562 | 1 UKHUT | c-plasminogen acti |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 184 | 36.2 | 618 | 2 A35827 | thrombin (EC 3.4.2 |
| 31 | 178.5 | 35.1 | 615 | 1 KRFU12 | coagulation factor |
| 32 | 174.5 | 34.4 | 946 | 1 A47299 | ror-related recept |
| 33 | 165.5 | 32.6 | 603 | 2 S28941 | coagulation factor |
| 34 | 163.5 | 32.2 | 558 | 2 UC5878 | plasma hyaluronan- |
| 35 | 163.5 | 32.2 | 937 | 2 A45082 | neurotrophic recep |
| 36 | 160 | 31.5 | 559 | 1 A29341 | c-plasminogen acti |
| 37 | 154 | 30.3 | 559 | 1 A35029 | t-plasminogen acti |
| 38 | 154 | 30.3 | 655 | 1 A46688 | hepatocyte growth |
| 39 | 146 | 28.7 | 442 | 1 UKRG | u-plasminogen acti |
| 40 | 143 | 28.1 | 433 | 1 UKMS | u-plasminogen acti |
| 41 | 142.5 | 28.1 | 560 | 1 JC4795 | plasma hyaluronan- |
| 42 | 142 | 28.0 | 685 | 1 A48289 | neurotrophic recep |
| 43 | 140 | 27.6 | 806 | 2 T18840 | hypothetical prote |
| 44 | 139.5 | 27.5 | 593 | 2 S45281 | coagulation factor |
| 45 | 138 | 27.2 | 432 | 1 S18932 | u-plasminogen acti |

ALIGNMENTS

RESULT 1
S00657
apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N.Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C.Species: Homo sapiens (man)
C.Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 08-Dec-2000
C.Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
R.McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Pless, G.M.; Scan
Nature 330, 132-137, 1987
A>Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A.Reference number: S00657; MUID:88039109; PMID:1670400
A.Accession: S00657
A.Molecule type: mRNA
A.Residues: 1-4548 <MCU>
A.Cross-references: GB:X06290; EMBL:X06696; NID:928619; PIDN:CAA29618.1; PID:928620
R.Bacon, D.L.; Pless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.;
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A>Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to
A.Reference number: A28017; MUID:87204109; PMID:3472206
A.Accession: A28017
A.Molecule type: Protein
A.Residues: 20-21, 'P', 23-34; 177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200; 292-314, 'W', 316-318
X', 4396-4401 <EAT>
R.Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A>Title: 5' control regions of the apolipoprotein(a) gene and members of the related plac
A.Reference number: A47277; MUID:93165698; PMID:7679504
A.Accession: A47277
A>Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-16 <RES>
A.Cross-references: GB:L07899; NID:9967973; PID:9967974
R.Malarecki, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Saccor
Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A>Title: Characterization by yeast artificial chromosome cloning of the linked apolipoprc
A.Reference number: A47233; MUID:93087573; PMID:1454851
A.Accession: I60906
A>Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-16 <RE2>
A.Cross-references: GB:M90078; NID:9178786; PIDN:AAA35547.1; PID:9551188
A.Note: apo(a) gene 1 (nomenclature of reference I52415)
A.Accession: A47233
A>Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-16 <RES>
A.Cross-references: GB:M90079; NID:9178784; PIDN:AAA35546.1; PID:9551187
R.Johnson, A.
Biochemistry 31, 3113-3118, 1992
A>Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated wit
A.Reference number: I52415; MUID:92207924; PMID:1554698
A.Accession: I52415

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RB3>
A:Cross-references: GB:M6877; NID:gi178780; PID:AA049909.1; PID:g553185
A>Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: I65286
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RB4>
A:Cross-references: GB:M6878; NID:gi178782; PID:AA051749.1; PID:g553186
C:Gene: LPA
C:GeneticB:
A:Cross-references: GDB:120699; OMIM:152200
A:Map position: 6q26-6q27
A>Note: several genes closely linked on chromosome 6 are identical in the first coding
re of kringle repeats
C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C:Keywords: hydrolase; Kringle; lipid binding; lipoprotein; serine proteinase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-45/8/Product: apolipoprotein(a) #status experimental <MAT>
F:28-105/Domain: kringle homology <KR1>
F:142-219/Domain: kringle homology <KR2>
F:256-333/Domain: kringle homology <KR3>
F:370-447/Domain: kringle homology <KR4>
F:484-561/Domain: kringle homology <KR5>
F:598-675/Domain: kringle homology <KR6>
F:712-789/Domain: kringle homology <KR7>
F:826-903/Domain: kringle homology <KR8>
F:940-1017/Domain: kringle homology <KR9>
F:1054-1131/Domain: kringle homology <KR10>
F:1168-1245/Domain: kringle homology <KR11>
F:1282-1359/Domain: kringle homology <KR12>
F:1396-1473/Domain: kringle homology <KR13>
F:1510-1587/Domain: kringle homology <KR14>
F:1624-1701/Domain: kringle homology <KR15>
F:1738-1815/Domain: kringle homology <KR16>
F:1852-1929/Domain: kringle homology <KR17>
F:1966-2043/Domain: kringle homology <KR18>
F:2080-2157/Domain: kringle homology <KR19>
F:2194-2271/Domain: kringle homology <KR20>
F:2308-2385/Domain: kringle homology <KR21>
F:2442-2499/Domain: kringle homology <KR22>
F:2556-2613/Domain: kringle homology <KR23>
F:2650-2727/Domain: kringle homology <KR24>
F:2764-2841/Domain: kringle homology <KR25>
F:2878-2955/Domain: kringle homology <KR26>
F:2992-3069/Domain: kringle homology <KR27>
F:3106-3183/Domain: kringle homology <KR28>
F:3220-3297/Domain: kringle homology <KR29>
F:3334-3411/Domain: kringle homology <KR30>
F:3448-3525/Domain: kringle homology <KR31>
F:3562-3639/Domain: kringle homology <KR32>
F:3676-3753/Domain: kringle homology <KR33>
F:3782-3859/Domain: kringle homology <KR34>
F:3896-3973/Domain: kringle homology <KR35>
F:4010-4087/Domain: kringle homology <KR36>
F:4124-4201/Domain: kringle homology <KR37>
F:4228-4307/Domain: kringle homology <KR38>
F:4328-4541/Domain: trypsin homology <TRY>

RESULT 2
B30848
plasmin (EC 3.4.21.7) precursor - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 31-Mar-1989 #sequence _revision 31-Mar-1989 #text_change 22-Jun-1999
C:Accession: B32869; B30848
R:Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A:Reference number: A32869; MUID:89174660; PMID:2925543
A:Accession: B32869
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-810 <TOM>
A:Cross-references: GB:J04697; NID:g342272; PID:AAA6901.1; PID:g342273
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-86/Domain: plasminogen-related protein precursor homology <PLPH>
F:1-181/Domain: signal sequence #status predicted <SIG>
F:181-262/Domain: kringle homology <KR1>
F:262-352/Domain: kringle homology <KR2>
F:352-454/Domain: kringle homology <KR3>
F:454-560/Domain: kringle homology <KR4>
F:561-803/Domain: trypsin homology <TRY>
F:449-73, 53-61, 103-181, 124-164, 152-176, 185-262, 188-316, 206-245, 234-257, 275-352, 296-335, 324-352/Domain: #status predicted
F:622, 665, 760/Active site: His, Asp, Ser #status predicted

| | Query Match | Similarity | Score | DB 2 | Length | 810 |
|------------|-------------|--|-------|------------|--------|------|
| Best Local | 83.7% | Pred. No. 1e-78 | | | | |
| Matches | 72 | Conservative | 4 | Mismatches | 10 | Gaps |
| | | | | | | |
| Qy | 1 | EODMFPNGKGYRKKKATTTVTGTCPEQEAADAEPPRHSHFPIGTNNAGLEKNYCGNPPGD | 60 | | | |
| | | | | | | |
| Db | 478 | EEDCMFNGKGYRKKKATTTVTGTCPEQEAADAEPPRHSHFPIGTNNAGLEKNYCGNPPGD | 537 | | | |
| | | | | | | |
| Qy | 61 | INGFWCTTMAPRKLFDYCDIPCLASS | 86 | | | |
| | | | | | | |
| Db | 538 | VGGFWCTTMAPRKLFDYCDIPCLASS | 563 | | | |
| | | | | | | |

RESULT 3
 PLHM
 plasmin (EC 3.4.21.7) precursor [validated] - human
 NAlternate names: plasminogen precursor [nismomel]
 NContains: angiotactin; microplasmin; plasminogen
 CSpecies: Homo sapiens (man)
 CDate: 24-Apr-1984 #sequence revision 02-Dec-1994 #text_change 15-Sep-2000
 CAccession: A55229; 152242; A26646; 162733; 184609; 503735; A009229; A04627; A04625; A04646
 R.Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
 J. Biol. Chem. 265, 6104-6111, 1990
 ATitle: Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system
 AReference number: A55229; MUID:90202879; PMID:2318848
 AAccession: A55229
 A.Molecule type: DNA
 A.Residues: 1-810 <PEP>
 A.Cross-references: GB:J05286; GB:M34276; NID:9190064; PIDN:AAA6013.1; PID:g387026
 A.Experimental source: leukocyte, lung fibroblast
 R.Margaret, N.; Bruno, L.; Fontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Tassi, P.
 Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
 ATitle: Definition of the transcription initiation site of human plasminogen gene in liver
 AReference number: 152242; MUID:91097523; PMID:2268308
 AAccession: 152242
 A.Status: translated from GB/EMBL/DBDJ
 A.Molecule type: DNA
 A.Residues: 1-16 <MAL>
 A.Cross-references: GB:M62890; NID:9190092; PIDN:AAA6454.1; PID:g553613
 R.Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
 FEBS Lett. 213, 254-260, 1987
 ATitle: Molecular cloning and characterization of a full-length cDNA clone for human plasminogen activator
 AReference number: A26646; MUID:87162490; PMID:3030813
 AAccession: A26646

A:Molecule type: mRNA
A:Residues: 1-471,'D',473-810 <FOR>
A:Cross-references: GB:X05199; NID:935530; PIDN:CAA28831.1; PID:935531
A:Experimental source: liver
R:Wallinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A:Reference number: 145961; PMID:85023311; PMID:6148961
A:Accession: 162738
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 292-471,'D',473-810 <MAL2>
A:Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031
A:Accession: 184609
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 367-619 <MAL3>
A:Cross-references: GB:K02921; NID:9190110; PIDN:AAA60123.1; PID:9190111
R:Brumsholtz, R.A.; Lerch, P.G.; Schallier, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1991
A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
A:Reference number: S03735; PMID:81212097; PMID:7238497
A:Accession: S03735
A:Molecule type: protein
A:Residues: 20-71,'E',73-76 <BRU>
R:Scott-Jensen, L.; Petersen, T.E.; Magnusson, S.
submitted to the Atlas July 1977
A:Reference number: A00929
A:Accession: A00929
A:Molecule type: protein
A:Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
R:Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A:Title: Primary structure of the B-chain of human plasmin.
A:Reference number: A04627; PMID:7725245; PMID:142009
A:Accession: A04627
A:Molecule type: protein
A:Residues: 581-810 <W1>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human pla
A:Reference number: A04625; PMID:75093329; PMID:122932
A:Accession: A04625
A:Molecule type: protein
A:Residues: 20-50,'Q',51-71,'E',73-85,87-100 <W12>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha
A:Reference number: A04626; PMID:76043692; PMID:126863
A:Accession: A04626
A:Molecule type: protein
A:Residues: 483-507,'E',509-604 <W13>
R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
A:Title: The primary structure of human plasminogen. II. The histidine loop of human pla
A:Reference number: A92125; PMID:3319248; PMID:4694729
A:Accession: A92125
A:Contents: annotation; active site
R:Groskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
A:Reference number: A92048; PMID:6924739; PMID:4420117
A:Accession: A92048
A:Contents: annotation; active site
R:Trexler, M.; Vail, Z.; Patsy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A:Reference number: A92382; PMID:82213905; PMID:6919539
A:Accession: A92382
A:Contents: annotation; omega-aminocarboxylic acid binding sites
R:Vail, Z.; Patsy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A:Reference number: A92458; PMID:85054794; PMID:6094526
A:Accession: A92458
A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site

R:Caio, Y.; Ji, R.W.; Davidson, D.; Schallier, J.; Marti, D.; Soehndel, S.; McCance, S.G.;
J. Biol. Chem. 271, 29461-29467, 1996
A:Title: Kringle domains of human angiotensin. Characterization of the anti-proliferative
A:Reference number: A58811; PMID:97067211; PMID:8910613
A:Accession: A58811
A:Contents: annotation
R:Jilka, H.R.; Uguw, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A:Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M
A:Reference number: A58812; PMID:9548733; PMID:9548733
A:Accession: A58812
A:Contents: annotation
R:Tulinsky, A.; Mulichak, A.M.
submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51341; PDB:1PK4
A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
R:Tulinsky, A.; Wu, T.P.
submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51486; PDB:1PK4
A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
R:Wu, T.P.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A:Reference number: A51911; PDB:1PKR
A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
R:Padmanabhan, K.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A:Reference number: A52408; PDB:1PKM
A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
R:Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A5244; PDB:1CEA
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R:Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A5245; PDB:1CEB
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R:Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A:Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 Å
A:Reference number: A58819; PMID:92031502; PMID:1657148
A:Accession: A58819
A:Contents: annotation
R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin
A:Reference number: A58818; PMID:92031503; PMID:1657149
A:Accession: A58818
A:Contents: annotation
R:de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.I.
Biochemistry 31, 270-279, 1992
A:Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4
A:Reference number: A39483; PMID:92118803; PMID:1310033
A:Accession: A39483
A:Contents: annotation; X-ray crystallography, 2.4 angstroms
R:Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A:Reference number: A65980; PDB:1KRN
A:Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A:Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A:Reference number: A63645; PMID:94237157; PMID:8181475
A:Accession: A63645
A:Contents: annotation; conformation by (1)H-NMR, residues 96-184
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminoge
A:Reference number: A58817; PMID:94237158; PMID:8181476
A:Accession: A58817
A:Contents: annotation; conformation by (1)H-NMR
C:Comment: plasminogen is synthesized by the kidney and is present in plasma and many oth
A:Comment: plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU at

d PIR:FGHUB).

C:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITTHA2) immediately after 580, resulting in two chains connected by two disulfide bonds. Without the inhibitor.

C:Comment: Microplasmin is formed by autocatalytic cleavage of plasmin under artificial conditions solid tumors.

C:Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiotensin. TC

C:Genetics:

A:Gene: GDB:PLG

A:Cross-references: GDB:119498; OMIM:173350

A:Map position: 6q26-6q27

A:Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529

C:Function:

A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the walls of the graafian follicle; also activates the urokinase-type plasminogen activator.

A:Pathway: fibrinolysis

C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology

C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-810/Product: plasminogen #status experimental <PRO>

F:20-96/Domain: activation peptide #status experimental <APT>

F:79-466/Product: angiotensin #status experimental <AST>

F:97-580/Domain: plasmin chain A #status experimental <CHA>

F:103-181/Domain: kringe homology <KR1>

F:185-262/Domain: kringe homology <KR2>

F:275-352/Domain: kringe homology <KR3>

F:377-454/Domain: kringe homology <KR4>

F:481-560/Domain: kringe homology <KR5>

F:550-580,581-810/Product: microplasmin #status experimental <MNT>

Query Match 84.6%; Score 430; DB 1; Length 810;

Best Local Similarity 82.4%; Pred. No. 1,7e-38;

Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EDDCMFGNGKGYRGKATVTGTPCOEWAQOEPRHSFTPGTNKVALEKNCRNPDGD 60

Db 478 EDDCMFGNGKGYRGKATVTGTPCOEWAQOEPRHSFTPGTNKVALEKNCRNPDGD 537

Qy 61 INGPWCYTNNPKRLFDYCDIPLCASS 85

Db 538 VGGPWCYTNNPKRLFDYCDIPLCASS 562

RESULT 4

B61545

plasmin (EC 3.4.21.7) precursor - sheep (fragments)

N:Alternate names: plasminogen

N:Contains: miniplasminogen

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999

C:Accession: B61545; S28200

R:Schaller, U.; Rickli, E.E.

Enzyme 40, 63-69, 1988

A:Title: Structural aspects of the plasminogen of various species.

A:Reference number: A61545; MUID:8905015; PMID:3168975

A:Accession: B61545

A:Molecule type: protein

A:Residues: 1-37;38-117 <SCH>

R:Schaller, U.; Straub, C.; Kaempfer, U.; Rickli, E.E.

Protein Seq. Data Anal. 5, 21-25, 1992

A:Title: Complete amino acid sequence of ovine miniplasminogen.

A:Reference number: S28200; MUID:9314995; PMID:1492092

A:Accession: S28200

A:Molecule type: protein

A:Residues: 118-460 <SC2>

C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringe; plasma; serine protease; z

F:1-37/Domain: activation peptide (fragment) #status experimental <APT>

F:38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT>

F:41-118/Domain: kringe homology <KR4>

F:118-460/Product: miniplasminogen #status experimental <MIN>

F:132-211/Domain: kringe homology <KR5>

F:226-460/Domain: plasmin chain B #status experimental <BCH>

F:231-453/Domain: trypsin homology <TRY>

F:272,315,410/Active site: His, Asp, Ser #status predicted

Query Match 81.9%; Score 416; DB 2; Length 460;

Best Local Similarity 82.6%; Pred. No. 3.1e-37;

Matches 71; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Qy 1 EDDCMFGNGKGYRGKATVTGTPCOEWAQOEPRHSFTPGTNKVALEKNCRNPDGD 60

Db 129 EDDCMFGNGKGYRGKATVTGTPCOEWAQOEPRHSFTPGTNKVALEKNCRNPDGD 188

Qy 61 INGPWCYTNNPKRLFDYCDIPLCASS 86

Db 189 VGGPWCYTNNPKRLFDYCDIPLCASS 214

RESULT 5

A61545

plasmin (EC 3.4.21.7) precursor - horse (fragments)

N:Alternate names: plasminogen

N:Contains: miniplasminogen

C:Species: Equus caballus (domestic horse)

C>Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997

C:Accession: A61545; S17527

R:Schaller, U.; Rickli, E.E.

Enzyme 40, 63-69, 1988

A:Title: Structural aspects of the plasminogen of various species.

A:Reference number: A61545; MUID:8905015; PMID:3168975

A:Accession: A61545

A:Molecule type: protein

A:Residues: 1-33;34-117 <SCH>

R:Schaller, U.; Straub, C.; Kaempfer, U.; Rickli, E.E.

Protein Seq. Data Anal. 4, 69-74, 1991

A:Title: Complete amino acid sequence of equine miniplasminogen.

A:Reference number: S17527; MUID:92052077; PMID:1946332

A:Accession: S17527

A:Molecule type: protein

A:Residues: 118-455 <SC2>

C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringe; plasma; serine protease; z

F:1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <PRO>

F:1-33/Domain: activation peptide (fragment) #status experimental <APT>

F:34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <MAT>

F:37-114/Domain: kringe homology <KR4>

F:118-455/Product: miniplasminogen #status experimental <MIN>

F:126-205/Domain: kringe homology <KR5>

F:226-455/Domain: plasmin chain B #status experimental <BCH>

F:226-448/Domain: trypsin homology <TRY>

F:267,310,405/Active site: His, Asp, Ser #status predicted

Query Match 81.7%; Score 415; DB 2; Length 455;

Best Local Similarity 80.2%; Pred. No. 3.9e-37;

Matches 69; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EDDCMFGNGKGYRGKATVTGTPCOEWAQOEPRHSFTPGTNKVALEKNCRNPDGD 60

Db 123 EDDCMFGNGKGYRGKATVTGTPCOEWAQOEPRHSFTPGTNKVALEKNCRNPDGD 182

Qy 61 INGPWCYTNNPKRLFDYCDIPLCASS 86

Db 183 VGGPWCYTNNPKRLFDYCDIPLCASS 208

RESULT 6

PLPG

plasmin (EC 3.4.21.7) precursor - pig (fragment)

N:Alternate names: plasminogen

N:Contains: miniplasminogen

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997

C:Accession: S03733; S03737; A25834

R.Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A>Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca
A:Reference number: S03733
A:Accession: S03733
A:Molecule type: protein
A:Residues: 1-560 <SCH>
R.Brunscholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A:Reference number: S03735; MUID:81212057; PMID:7238497
A:Accession: S03737
A:Molecule type: protein
A:Residues: 1-57 <BRU>
R.Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A>Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A:Reference number: A25834; MUID:85203907; PMID:3846533
A:Accession: A25834
A:Molecule type: protein
A:Residues: 450-790 <MAR>
C:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A:Pathway: fibrinolysis
C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringe; plasma; serine prote
F.1-790/Product: plasminogen #status predicted <PRO>
F.1-77/Domains: plasminogen-related protein precursor homology (fragment) <PLPH>
F.1-77/Domains: activation peptide #status predicted <APT>
F.78-560/Product: plasmin chain A #status predicted <ACH>
F.84-162/Domains: kringe homology <KR1>
F.166-243/Domains: kringe homology <KR2>
F.256-333/Domains: kringe homology <KR3>
F.358-435/Domains: kringe homology <KR4>
F.450-790/Product: miniplasminogen #status experimental <MIN>
F.461-540/Domains: kringe homology <KR5>
F.561-790/Product: plasmin chain B #status experimental <BCH>
F.561-783/Domains: trypsin homology <TRY>
F.330-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305
bonds: #status predicted
F.602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 80.5%; Score 409; DB 1; Length 790;
Best Local Similarity 80.0%; Pred. No. 3e-36; Mismatches 12; Indels 0; Gaps 0;
Matches 68; Conservative 5;

QY 2 ODCMFGNGKGYRGKATVTTGTPCOEWAQEPHRSFTPTGNTKAGLEKNTYCRNPDGD 61
DB 459 EDCMFGNGKGYRGKATVTTGTPCOEWAQEPHRSFTPTGNTKAGLEKNTYCRNPDGD 518

QY 62 NGPWCTYTNPRKLFYDCDIPLCASS 86
DB 519 NGPWCTYTNPRKLFYDCDIPLCASS 543

RESULT 7

PLMS
plasmin (EC 3.4.21.7) precursor - mouse
N:Contains: angiotatin; plasminogen
C:Species: Mus musculus (house mouse)
C>Date: 20-Sep-1991 #sequence revision 01-Nov-1996 #text_change 18-Jun-1999
R:Accession: A38514; S48202; S48203
R:Idgen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics 8, 49-61, 1990
A>Title: Characterization of the cDNA coding for mouse plasminogen and localization of
A:Reference number: A38514; MUID:91184812; PMID:2081600
A:Accession: A38514
A:Molecule type: mRNA
A:Residues: 1-812 <DEG>
A:Cross-references: GB:J04766; NID:g200402; PIDN:AAAS0168.1; PID:g200403
R:Idgen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994

A>Title: Characterization of the murine plasma fibrinolytic system.
A:Reference number: S48202; MUID:95010076; PMID:7523120
A:Accession: S48202
A:Molecule type: protein
A:Residues: 20-25 <LIJ>
A:Accession: S48203
A:Molecule type: protein
A:Residues: 22-27 <LI2>
C:Comment: plasminogen is synthesized by the kidney and is present in plasma and many oth
C:Comment: plasminogen is converted into plasmin by plasminogen activators, both plasmin
mediately after dissociation from the clots. In the presence of the inhibitor, the activat
e inhibitor, the activation involves also removal of the activation peptide.
C:Comment: Streptolysin 1 (see PIR:KCMS1) acts on plasminogen to produce angiotatin. Tog
eful in treating solid tumors.
C:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen acti
A:Pathway: fibrinolysis
C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology;
C:Keywords: angiotatin; plasminogen; blood; duplication; fibrinolysis; glycoprotein; hydrc
F.1-96/Domains: plasminogen-related protein precursor homology <PLPH>
F.1-19/Domains: signal sequence #status predicted <SIG>
F.20-812/Product: plasminogen #status predicted <PRO>
F.20-96/Domains: activation peptide #status predicted <APT>
F.79-466/Product: angiotatin #status predicted <AST>
F.97-581,582-812/Product: plasmin #status predicted <MAT>
F.97-581/Domains: chain A #status predicted <ACH>
F.103-181/Domains: kringe homology <KR1>
F.185-262/Domains: kringe homology <KR2>
F.275-352/Domains: kringe homology <KR3>
F.377-454/Domains: kringe homology <KR4>
F.481-560/Domains: kringe homology <KR5>
F.582-812/Domains: chain B #status predicted <BCH>
F.582-805/Domains: trypsin homology <TRY>
F.49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,324
bonds: #status predicted
F.78-79/Cleavage site: Glu-Aen (stromelysin 1) #status predicted
F.136,308/Binding site: carbohydrate (Aen) (covalent) #status predicted
F.466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
F.581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
F.624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 79.9%; Score 406; DB 1; Length 812;
Best Local Similarity 79.1%; Pred. No. 6.5e-36;
Matches 68; Conservative 4; Mismatches 14; Indels 0; Gaps 0;
Matches 68; Conservative 4;

QY 1 EDCMFGNGKGYRGKATVTTGTPCOEWAQEPHRSFTPTGNTKAGLEKNTYCRNPDGD 60
DB 478 EDCMFGNGKGYRGKATVTTGTPCOEWAQEPHRSFTPTGNTKAGLEKNTYCRNPDGD 537

QY 61 INGPWCYTNPRKLFYDCDIPLCASS 86
DB 538 INGPWCYTNPRKLFYDCDIPLCASS 563

RESULT 8

PIBO
plasmin (EC 3.4.21.7) precursor - bovine
N:Alternate names: plasminogen
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1987 #sequence revision 28-Apr-1995 #text_change 18-Jun-1999
R:Accession: S45046; A25835; I45961; S03736
R:Berghlund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A:Description: Cloning and characterization of the bovine plasminogen cDNA.
A:Reference number: S45046
A:Accession: S45046
A:Molecule type: mRNA
A:Residues: 1-812 <BBR>
A:Cross-references: EMBL:X79402; NID:g494962; PIDN:CAA55939.1; PID:g494963
A:Experimental source: liver
A>Note: It is uncertain whether Met-1 or Met-8 is the initiator
R.Schaller, U.; Moser, P.W.; Danneberg-Muller, G.A.K.; Roesselet, S.J.; Kaempfer, U.; Rickl

Eur. J. Biochem. 149, 267-278, 1985
 A/Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasmin
 A/Reference number: A25835; MUID:85203906; PMID:3846532
 A/Accession: A25835
 A/Molecule type: protein
 A/Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
 R/Malinowski, D. P.; Sadler, J. E.; Davie, E. W.
 Biochemistry 23, 4243-4250, 1984
 A/Title: Characterization of a complementary deoxyribonucleic acid coding for human and
 A/Reference number: 145961; MUID:85023311; PMID:6148961
 A/Accession: 145961
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 706-743, 'R', 745-812 <MAL>
 A/Cross-references: GB:K02935; NID:g163551; PID:AAA0714.1; PID:g163552
 R/Brunsholz, R. A.; Lersch, P. G.; Schaller, J.; Rickli, E. E.; Legier, W.; Manneberg, M.;
 Eur. J. Biochem. 114, 465-470, 1991
 A/Title: Completion of the primary structure of the N-terminal CNBr fragments of human,
 A/Reference number: S03735; MUID:81212097; PMID:7238497
 A/Accession: S03735
 A/Molecule type: protein
 A/Residues: 27-83 <BRU>
 C/Function:
 A/Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 as the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A/Pathway: fibrinolysis
 C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C/Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:8-103/Domain: plasminogen-related protein precursor homology <PLPH>
 F:27-812/Product: activation peptide #status experimental <PRO>
 F:27-103/Domain: activation peptide #status experimental <APR>
 F:104-583-584-812/Product: plasmin #status experimental <MAT>
 F:110-583/Domain: plasmin chain A #status experimental <ACH>
 F:110-188/Domain: kringle homology <KR1>
 F:192-269/Domain: kringle homology <KR2>
 F:282-359/Domain: kringle homology <KR3>
 F:384-461/Domain: kringle homology <KR4>
 F:485-564/Domain: kringle homology <KR5>
 F:584-812/Domain: plasmin chain B #status experimental <BCH>
 F:584-805/Domain: trypsin homology <TRY>
 F:56-80, 60-68, 110-188, 131-171, 159-183, 192-269, 195-323, 213-252, 241-264, 282-359, 303-342, 33
 bonds: #status predicted
 F:315/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:365/Binding site: carboxylate (Ser) (covalent) #status experimental
 F:624, 667, 762/Active site: His, Asp, Ser #status predicted
 Query Match 79.9%; Score 406; DB 1; Length 812;
 Best Local Similarity 77.9%; Pred. No. 6, 5e-36;
 Matches 67; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
 QY 1 EDDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSFTPGTNKAGLEKNYCRNPDGD 60
 DB 482 EADCMIGTGSYRGKATTAAGVPCQEMAAQEPHRSIFTPETNPOSGLEKNYCRNPDGD 541
 QY 61 INGPWCYTNNPKRLFDYCDIPLCAS 86
 DB 542 VNGPWCTTNNPKRPFYCDVPCQESS 567

RESULT 9
 146260
 Plasmin (EC 3.4.21.7) precursor - western European hedgehog
 C/Species: Erinaceus europaeus (western European hedgehog)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C/Accession: 146260
 R/Jawm, R. M.; Boommark, N. W.; Schwartz, K.; Lindahl, G. E.; Wade, D. P.; Byrne, C. D.; Fong
 J. Biol. Chem. 270, 24004-24009, 1995
 A/Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot
 A/Reference number: 146259; MUID:96025778; PMID:7552597
 A/Accession: 146260
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA

A/Residues: 1-810 <LAW>
 A/Cross-references: EMBL:U33171; NID:g1046360; PID:g1046361
 C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
 C/Keywords: hydrolase; serine proteinase
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 F:103-181/Domain: kringle homology <KR1>
 F:185-262/Domain: kringle homology <KR2>
 F:275-352/Domain: kringle homology <KR3>
 F:379-456/Domain: kringle homology <KR4>
 F:482-561/Domain: kringle homology <KR5>
 F:582-803/Domain: trypsin homology <TRY>
 Query Match 76.4%; Score 388; DB 2; Length 810;
 Best Local Similarity 77.6%; Pred. No. 5, 7e-34;
 Matches 66; Conservative 3; Mismatches 16; Indels 0; Gaps 0;
 QY 1 EDDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSFTPGTNKAGLEKNYCRNPDGD 60
 DB 479 EDDCIIDNGKGYRGVATTAAGTPOCWAQEPHRSIFTPETNPRADQENYCRNPDGD 538
 QY 61 INGPWCYTNNPKRLFDYCDIPLCAS 85
 DB 539 ANGPWCYTNNPKRLFDYCDIPLCAS 563

RESULT 10
 A40522
 Plasmin (EC 3.4.21.7) precursor - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
 C/Accession: A40522
 R/Kanalaas, U. J.; Makker, S. P.
 J. Biol. Chem. 266, 10825-10829, 1991
 A/Title: Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor s
 A/Reference number: A40522; MUID:9150378; PMID:1645711
 A/Accession: A40522
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-169 <VAN>
 A/Cross-references: GB:M62832; NID:G206215; PID:AAA41884.1; PID:9554488
 A/Note: the authors translated the codon TGT for residue 76 as Ala
 C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:24-112/Domain: kringle homology <KR>
 F:24-112, 55-95, 83-107/Disulfide bonds: #status predicted
 Query Match 47.9%; Score 243.5; DB 2; Length 169;
 Best Local Similarity 48.2%; Pred. No. 4, 9e-19;
 Matches 41; Conservative 12; Mismatches 31; Indels 1; Gaps 1;
 QY 2 QDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSFTPGTNKAGLEKNYCRNPDGD 61
 DB 32 QECYQNGKGSYRGTSITTTGKKCGSWMTPHSHK-TPANPPDSGLEKNYCRNPDNDQ 90
 QY 62 NGPWCTTNNPKRLFDYCDIPLCAS 86
 DB 91 RGPWCFTTDPVSVMWEYCNMKRCSET 115

RESULT 11
 JCS061
 macrophage-stimulating protein 1 precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000
 C/Accession: JCS061
 R/Onishi, K.; Itama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamauchi, I.; Takaue, N.
 Biochem. Biophys. Res. Commun. 227, 273-280, 1996
 A/Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in t
 A/Reference number: JCS061; MUID:97011126; PMID:8858136
 A/Accession: JCS061
 A/Molecule type: mRNA
 A/Residues: 1-716 <OHS>
 A/Cross-references: EMBL:X95096; NID:g1669718; PID:CAA64473.1; PID:g1669719

A;Residues: 1-711 <HA1>
A;Cross-references: GB:M74179

A;Cross-references: GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
C;Genetics:

A;introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 47
 C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C;Superfamily: hepatocyte growth factor: kringle homology; trypsin homology
 C;Keywords: duplication; glycoprotein; growth factor; kringle
 F;1-31/Domain: signal sequence #status predicted <SIG>
 F;19-488-489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>
 F;19-483/Domain: alpha chain #status experimental <ACH>
 F;110-186/Domain: kringle homology <KR1>
 F;191-268/Domain: kringle homology <KR2>
 F;392-370/Domain: kringle homology <KR3>
 F;379-457/Domain: kringle homology <KR4>
 F;484-711/Domain: beta chain #status experimental <BCH>
 F;489-709/Domain: trypsin homology <TRY>
 F;72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.1%; Score 239.5; DB 1; Length 716;

Best Local Similarity 48.8%; Pred. No. 5.6e-18;
 Matches 40; Conservative 14; Mismatches 27; Indels 1; Gaps 1;

QY 2 QDCMFGNGKGRGKATTTVTGTPCEWMAQEPHRSSTFGTNKMGLEKNYGRNPDGDI 61

DB 377 EGCYHSGEGYRGSVSKTRKGVCCQHWSSSTPHK-PQFTPTSAPOAGLEAFGRNPDGDS 435

QY 62 NGPWCYTNNPRKLEFDYCDIPLC 83

DB 436 HGPWCYTLDPDILFDYCALQRC 457

RESULT 15

T18518

apolipoprotein(a) - western European hedgehog (fragment)

C;Species: Eritaceus europaeus (western European hedgehog)

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999

C;Accession: T18518

R;Lawm, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong

J. Biol. Chem. 270, 24004-24009, 1995

A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein

A;Reference number: 146259; PMID:96025778; PMID:7592597

A;Accession: T18518

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-2869 <LAW>

A;Cross-references: EMBL:U33170; NID:G1046358; PID:G1046359; PIDN:AAC48522.1

A;Experimental source: liver

C;Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, con-

ent apolipoprotein(a).

Query Match 47.0%; Score 239; DB 2; Length 2869;

Best Local Similarity 50.6%; Pred. No. 2.5e-17;
 Matches 43; Conservative 9; Mismatches 31; Indels 2; Gaps 2;

QY 2 QDCMFGNGKGRGKATTTVTGTPCEWMAQEPHRSSTFGTNKMGLEKNYGRNPDGDI 61

DB 2589 EOCLENGENYQGNMAITVSGPCQGRKQTPRHHE-YTPENYPSKULFGNYGRNPDGDI 2647

QY 62 NGPWCYTNNPRKLEFDYCDIPLCASS 86

DB 2648 -APWCYTNNPRKLEFDYCDIPLCASS 2671

Search completed: January 12, 2004, 17:26:24
 Job time: 11.6391 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:17:22 : Search time 7.43609 Seconds

(without alignments)
543.874 Million cell updates/sec

Title: US-10-088-548-8

Perfect score: 508

Sequence: 1 EDDCMFGNGKGYRGKATTV.....YTMNPRKLPDYCDIPLGASS 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 508 | 100.0 | 4548 | 1 | APOA_HUMAN |
| 2 | 432 | 85.0 | 810 | 1 | PLMN_MACMU |
| 3 | 430 | 84.6 | 810 | 1 | PLMN_HUMAN |
| 4 | 425 | 83.7 | 333 | 1 | PLMN_CANFA |
| 5 | 416 | 81.9 | 343 | 1 | PLMN_SHEEP |
| 6 | 415 | 81.7 | 338 | 1 | PLMN_HORSE |
| 7 | 413 | 81.3 | 812 | 1 | PLMN_MOUSE |
| 8 | 409 | 80.5 | 790 | 1 | PLMN_PIG |
| 9 | 406 | 79.9 | 812 | 1 | PLMN_BOVIN |
| 10 | 388 | 76.4 | 810 | 1 | PLMN_BRIEU |
| 11 | 243.5 | 47.9 | 169 | 1 | PLMN_RAT |
| 12 | 241.5 | 47.5 | 711 | 1 | HGFL_HUMAN |
| 13 | 239.5 | 47.1 | 716 | 1 | HGFL_MOUSE |
| 14 | 236 | 46.5 | 1420 | 1 | APOA_MACMU |
| 15 | 234.5 | 46.2 | 728 | 1 | HGF_HUMAN |
| 16 | 227.5 | 44.8 | 728 | 1 | HGF_MOUSE |
| 17 | 227.5 | 44.8 | 728 | 1 | HGF_RAT |
| 18 | 206.5 | 40.6 | 625 | 1 | THRB_BOVIN |
| 19 | 199.5 | 39.3 | 325 | 1 | PLMN_PETMA |
| 20 | 198.5 | 39.1 | 943 | 1 | ROR2_HUMAN |
| 21 | 196.5 | 38.7 | 944 | 1 | ROR2_MOUSE |
| 22 | 195 | 38.4 | 617 | 1 | THRB_RAT |
| 23 | 191.5 | 37.7 | 622 | 1 | THRB_HUMAN |
| 24 | 188.5 | 37.1 | 724 | 1 | ROR2_DROME |
| 25 | 187 | 36.8 | 562 | 1 | THRB_MOUSE |
| 26 | 184 | 36.2 | 618 | 1 | THRB_MOUSE |
| 27 | 178.5 | 35.1 | 615 | 1 | FAI2_HUMAN |
| 28 | 170 | 33.5 | 566 | 1 | TPA_BOVIN |
| 29 | 165.5 | 32.6 | 603 | 1 | FAI2_CAVPO |
| 30 | 163.5 | 32.2 | 937 | 1 | ROR1_HUMAN |
| 31 | 163.5 | 32.2 | 937 | 1 | ROR1_MOUSE |
| 32 | 160 | 31.5 | 461 | 1 | KRM2_MOUSE |
| 33 | 159.5 | 31.4 | 473 | 1 | KRM1_MOUSE |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 159.5 | 31.4 | 473 | 1 | KRM1_RAT | Q92484 ratius norv |
| 35 | 159 | 31.3 | 462 | 1 | KRM2_HUMAN | Q8ncw0 homo sapien |
| 36 | 159 | 31.3 | 559 | 1 | TPA_MOUSE | P11214 mus musculu |
| 37 | 156.5 | 30.8 | 475 | 1 | KRM1_HUMAN | Q96m88 homo sapien |
| 38 | 154.5 | 30.4 | 452 | 1 | KRM1_XENLA | Q90y90 xenopus lae |
| 39 | 154 | 30.3 | 559 | 1 | TPA_RAT | P19637 ratius norv |
| 40 | 154 | 30.3 | 655 | 1 | HGFL_HUMAN | Q04756 homo sapien |
| 41 | 146 | 28.7 | 442 | 1 | UROK_PIG | P04185 sus scrofa |
| 42 | 143 | 28.1 | 433 | 1 | UROK_MOUSE | P06869 mus musculu |
| 43 | 142 | 28.0 | 685 | 1 | ROR1_DROME | Q24488 drosophila |
| 44 | 139.5 | 27.5 | 593 | 1 | FAI2_BOVIN | P98140 bos taurus |
| 45 | 138 | 27.2 | 432 | 1 | UROK_RAT | P29598 ratius norv |

ALIGNMENTS

RESULT 1
APOA_HUMAN STANDARD; PRT; 4548 AA.
AC P08519;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
GN LpA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=8803109; PubMed=3670400;
RA Mleas J.W., Tomlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,
RC Salonen E.-M., Jauhainen M., Zardi L., Vaheri A., Einholm C.,
RT "CDNA sequence of human apolipoprotein(a) is homologous to
RT plasminogen.";
RT Nature 330:132-137(1987).
RN [2]
RP SERINE PROTEASE ACTIVITY.
RX MEDLINE=90076123; PubMed=2531657;
RA Salonen E.-M., Jauhainen M., Zardi L., Vaheri A., Einholm C.,
RT "Lipoprotein(a) binds to fibronectin and has serine proteinase
RL activity capable of cleaving it.";
RL EMBO J. 8:4035-4040(1989).
RN [3]
RP REVIEW.
RX MEDLINE=90049223; PubMed=2530631;
RA Utermann G.;
RT "The mysteries of lipoprotein(a).";
RL Science 246:904-910(1989).
RN [4]
RP CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
RX MEDLINE=21303595; PubMed=11294842;
RA Garner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.;
RT "Structural elucidation of the N- and O-glycans in human
RT apolipoprotein(a): role of O-glycans in conferring protease
RT resistance.";
RL J. Biol. Chem. 276:22200-22208(2001).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
RX MEDLINE=96217891; PubMed=8642595;
RA Mikol V., Lograsso P.V., Boettcher B.R.;
RT "Crystal structures of apolipoprotein(a) kringle IV37 free and
RT complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic
RL acid: existence of novel and expected binding modes.";
RL J. Mol. Biol. 256:751-761(1996).
RN [6]
RP VARIANT ARG-4193.
RX MEDLINE=95002201; PubMed=7918682;
RA Scannu A.M., Pfaffinger D., Lee J.C., Himan J.;
RT "A single point mutation (Trp72-->Arg) in human apo(a) kringle 4-37
RT associated with a lysine binding defect in Lp(a)." ;

RL Biochim. Biophys. Acta 1227:41-45 (1994).

CC -1- FUNCTION: Apo(a) is the main constituent of lipoprotein(a) (Lp(a)). It has serine proteinase activity and is able of autoproteolysis. Inhibits tissue-type plasminogen activator 1. Lp(a) may be a ligand for megalin/Gp 330.

CC -1- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and decorin.

CC -1- PTM: N- and O-glycosylated. The N-glycans are complex biantennary structures present in either a mono- or disialylated state. The O-glycans are mostly (80%) represented by the monosialylated core type I structure, NeuAcalpha2-3Galbeta1-3GalNAc, with smaller amounts of disialylated and non-sialylated O-glycans also detected.

CC -1- DISEASE: Elevated plasma concentrations of apo(a) and its naturally occurring proteolytic fragments are correlated with atherosclerosis. Homology with plasminogen kringle IV and V is thought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrin(ogen) binding.

CC MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved, leading to the formation of the so called mini-lp(a). Apo(a) fragments accumulate in atherosclerotic lesions, where they may promote thrombogenesis. O-glycosylation may limit the extent of proteolytic fragmentation.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY. -1- SIMILARITY: Contains 38 kringle domains.

CC -----

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CC -----

CC EMBL: X06290; CAA29618.1; -.

CC PIR: S00657; S00657.

CC PDB: 1I71; 13-JUN-01.

CC PDB: 1JFN; 28-JUN-02.

CC PDB: 1KIV; 18-MAY-99.

CC PDB: 3KIV; 18-MAY-99.

CC PDB: 4KIV; 18-MAY-99.

CC MEROPS: S01.226; -.

CC Genew: HGNC:6667; LPA.

CC MIM: 152200; -.

CC DR GO: GO:0004865; P: endopeptidase inhibitor activity; TAS.

CC DR GO: GO:0008015; P: circulation; TAS.

CC DR GO: GO:0009405; P: pathogenesis; TAS.

CC DR InterPro: IPR001314; Chymotrypsin.

CC DR InterPro: IPR000001; Kringle.

CC DR InterPro: IPR001254; Ser protease_Try.

CC Pfam: PF00051; kringle_38.

CC Pfam: PF00089; trypsin_1.

CC PRINTS: PR00722; CHYMOTRYPSIN.

CC PRINTS: PR00018; KRINGLE.

CC ProDom: PD000395; Kringle_38.

CC SMART: SM00130; KR: 38.

CC SMART: SM00020; TRY: SRC: 1.

CC PROSITE: PS00021; KRINGLE_1; 38.

CC PROSITE: PS00070; KRINGLE_2; 38.

CC PROSITE: PS00240; TRYPsin DOM; 1.

CC PROSITE: PS00134; TRYPsin HIS; 1.

CC PROSITE: PS00135; TRYPsin SER; 1.

CC HydroLase: Serine protease; Lipid transport; Plasma; Glycoprotein; Kringle; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure.

KW Kringl; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure.

FT CHAIN 1 19

FT SIGLVL 1 19

FT CHAIN 20 4548

FT DOMAIN 20 130

FT DOMAIN 131 244

FT DOMAIN 245 358

FT DOMAIN 359 472

FT DOMAIN 473 586

FT DOMAIN 587 700

FT DOMAIN 701 814

APOLIPOPROTEIN(A).

KRINGLE TYPE IV, 1.

KRINGLE TYPE IV, 2.

KRINGLE TYPE IV, 3.

KRINGLE TYPE IV, 4.

KRINGLE TYPE IV, 5.

KRINGLE TYPE IV, 6.

KRINGLE TYPE IV, 7.

| FT | DOMAIN | 815 | 928 | KRINGLE TYPE IV, 8. |
|----|----------|-------|-------|-----------------------|
| FT | DOMAIN | 929 | 1042 | KRINGLE TYPE IV, 9. |
| FT | DOMAIN | 1043 | 1156 | KRINGLE TYPE IV, 10. |
| FT | DOMAIN | 1157 | 1270 | KRINGLE TYPE IV, 11. |
| FT | DOMAIN | 1271 | 1384 | KRINGLE TYPE IV, 12. |
| FT | DOMAIN | 1385 | 1498 | KRINGLE TYPE IV, 13. |
| FT | DOMAIN | 1499 | 1612 | KRINGLE TYPE IV, 14. |
| FT | DOMAIN | 1613 | 1726 | KRINGLE TYPE IV, 15. |
| FT | DOMAIN | 1727 | 1840 | KRINGLE TYPE IV, 16. |
| FT | DOMAIN | 1841 | 1954 | KRINGLE TYPE IV, 17. |
| FT | DOMAIN | 1955 | 2068 | KRINGLE TYPE IV, 18. |
| FT | DOMAIN | 2069 | 2182 | KRINGLE TYPE IV, 19. |
| FT | DOMAIN | 2183 | 2296 | KRINGLE TYPE IV, 20. |
| FT | DOMAIN | 2297 | 2410 | KRINGLE TYPE IV, 21. |
| FT | DOMAIN | 2411 | 2524 | KRINGLE TYPE IV, 22. |
| FT | DOMAIN | 2525 | 2638 | KRINGLE TYPE IV, 23. |
| FT | DOMAIN | 2639 | 2752 | KRINGLE TYPE IV, 24. |
| FT | DOMAIN | 2753 | 2866 | KRINGLE TYPE IV, 25. |
| FT | DOMAIN | 2867 | 2980 | KRINGLE TYPE IV, 26. |
| FT | DOMAIN | 2981 | 3094 | KRINGLE TYPE IV, 27. |
| FT | DOMAIN | 3095 | 3208 | KRINGLE TYPE IV, 28. |
| FT | DOMAIN | 3209 | 3322 | KRINGLE TYPE IV, 29. |
| FT | DOMAIN | 3323 | 3436 | KRINGLE TYPE IV, 30. |
| FT | DOMAIN | 3437 | 3550 | KRINGLE TYPE IV, 31. |
| FT | DOMAIN | 3551 | 3664 | KRINGLE TYPE IV, 32. |
| FT | DOMAIN | 3665 | 3778 | KRINGLE TYPE IV, 33. |
| FT | DOMAIN | 3779 | 3893 | KRINGLE TYPE IV, 34. |
| FT | DOMAIN | 3894 | 4007 | KRINGLE TYPE IV, 35. |
| FT | DOMAIN | 4008 | 4122 | KRINGLE TYPE IV, 36. |
| FT | DOMAIN | 4123 | 4237 | KRINGLE TYPE IV, 37. |
| FT | DOMAIN | 4238 | 4352 | KRINGLE TYPE IV, 38. |
| FT | DOMAIN | 4353 | 4467 | KRINGLE TYPE IV, 39. |
| FT | ACT SITE | 4468 | 4582 | KRINGLE TYPE IV, 40. |
| FT | ACT SITE | 4583 | 4697 | KRINGLE TYPE IV, 41. |
| FT | ACT SITE | 4698 | 4812 | KRINGLE TYPE IV, 42. |
| FT | ACT SITE | 4813 | 4927 | KRINGLE TYPE IV, 43. |
| FT | ACT SITE | 4928 | 5042 | KRINGLE TYPE IV, 44. |
| FT | ACT SITE | 5043 | 5157 | KRINGLE TYPE IV, 45. |
| FT | ACT SITE | 5158 | 5272 | KRINGLE TYPE IV, 46. |
| FT | ACT SITE | 5273 | 5387 | KRINGLE TYPE IV, 47. |
| FT | ACT SITE | 5388 | 5502 | KRINGLE TYPE IV, 48. |
| FT | ACT SITE | 5503 | 5617 | KRINGLE TYPE IV, 49. |
| FT | ACT SITE | 5618 | 5732 | KRINGLE TYPE IV, 50. |
| FT | ACT SITE | 5733 | 5847 | KRINGLE TYPE IV, 51. |
| FT | ACT SITE | 5848 | 5962 | KRINGLE TYPE IV, 52. |
| FT | ACT SITE | 5963 | 6077 | KRINGLE TYPE IV, 53. |
| FT | ACT SITE | 6078 | 6192 | KRINGLE TYPE IV, 54. |
| FT | ACT SITE | 6193 | 6307 | KRINGLE TYPE IV, 55. |
| FT | ACT SITE | 6308 | 6422 | KRINGLE TYPE IV, 56. |
| FT | ACT SITE | 6423 | 6537 | KRINGLE TYPE IV, 57. |
| FT | ACT SITE | 6538 | 6652 | KRINGLE TYPE IV, 58. |
| FT | ACT SITE | 6653 | 6767 | KRINGLE TYPE IV, 59. |
| FT | ACT SITE | 6768 | 6882 | KRINGLE TYPE IV, 60. |
| FT | ACT SITE | 6883 | 6997 | KRINGLE TYPE IV, 61. |
| FT | ACT SITE | 6998 | 7112 | KRINGLE TYPE IV, 62. |
| FT | ACT SITE | 7113 | 7227 | KRINGLE TYPE IV, 63. |
| FT | ACT SITE | 7228 | 7342 | KRINGLE TYPE IV, 64. |
| FT | ACT SITE | 7343 | 7457 | KRINGLE TYPE IV, 65. |
| FT | ACT SITE | 7458 | 7572 | KRINGLE TYPE IV, 66. |
| FT | ACT SITE | 7573 | 7687 | KRINGLE TYPE IV, 67. |
| FT | ACT SITE | 7688 | 7802 | KRINGLE TYPE IV, 68. |
| FT | ACT SITE | 7803 | 7917 | KRINGLE TYPE IV, 69. |
| FT | ACT SITE | 7918 | 8032 | KRINGLE TYPE IV, 70. |
| FT | ACT SITE | 8033 | 8147 | KRINGLE TYPE IV, 71. |
| FT | ACT SITE | 8148 | 8262 | KRINGLE TYPE IV, 72. |
| FT | ACT SITE | 8263 | 8377 | KRINGLE TYPE IV, 73. |
| FT | ACT SITE | 8378 | 8492 | KRINGLE TYPE IV, 74. |
| FT | ACT SITE | 8493 | 8607 | KRINGLE TYPE IV, 75. |
| FT | ACT SITE | 8608 | 8722 | KRINGLE TYPE IV, 76. |
| FT | ACT SITE | 8723 | 8837 | KRINGLE TYPE IV, 77. |
| FT | ACT SITE | 8838 | 8952 | KRINGLE TYPE IV, 78. |
| FT | ACT SITE | 8953 | 9067 | KRINGLE TYPE IV, 79. |
| FT | ACT SITE | 9068 | 9182 | KRINGLE TYPE IV, 80. |
| FT | ACT SITE | 9183 | 9297 | KRINGLE TYPE IV, 81. |
| FT | ACT SITE | 9298 | 9412 | KRINGLE TYPE IV, 82. |
| FT | ACT SITE | 9413 | 9527 | KRINGLE TYPE IV, 83. |
| FT | ACT SITE | 9528 | 9642 | KRINGLE TYPE IV, 84. |
| FT | ACT SITE | 9643 | 9757 | KRINGLE TYPE IV, 85. |
| FT | ACT SITE | 9758 | 9872 | KRINGLE TYPE IV, 86. |
| FT | ACT SITE | 9873 | 9987 | KRINGLE TYPE IV, 87. |
| FT | ACT SITE | 9988 | 10102 | KRINGLE TYPE IV, 88. |
| FT | ACT SITE | 10103 | 10217 | KRINGLE TYPE IV, 89. |
| FT | ACT SITE | 10218 | 10332 | KRINGLE TYPE IV, 90. |
| FT | ACT SITE | 10333 | 10447 | KRINGLE TYPE IV, 91. |
| FT | ACT SITE | 10448 | 10562 | KRINGLE TYPE IV, 92. |
| FT | ACT SITE | 10563 | 10677 | KRINGLE TYPE IV, 93. |
| FT | ACT SITE | 10678 | 10792 | KRINGLE TYPE IV, 94. |
| FT | ACT SITE | 10793 | 10907 | KRINGLE TYPE IV, 95. |
| FT | ACT SITE | 10908 | 11022 | KRINGLE TYPE IV, 96. |
| FT | ACT SITE | 11023 | 11137 | KRINGLE TYPE IV, 97. |
| FT | ACT SITE | 11138 | 11252 | KRINGLE TYPE IV, 98. |
| FT | ACT SITE | 11253 | 11367 | KRINGLE TYPE IV, 99. |
| FT | ACT SITE | 11368 | 11482 | KRINGLE TYPE IV, 100. |

SEQUENCE 4548 AA; 50133 MW; 96921BE96A465CSF CRC64; /FTID=VAR 006633.

Query Match 100.0%; Score 508; DB 1; Length 4548; Best Local Similarity 100.0%; Pred. No. 3.2e-48; Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYGKATVTGTPCOEMAAOEPHRSSTIIPGINKAGLEKXVCRRPDD 60

DB 4225 EODCMFGNGKGYGKATVTGTPCOEMAAOEPHRSSTIIPGINKAGLEKXVCRRPDD 4284

QY 61 INGPWCYTNNPRKLPDYCDIPICASS 86

DB 4285 INGPWCYTNNPRKLPDYCDIPICASS 4310

RESULT 2

PLNN MACMU STANDARD; PRT; 810 AA.

AC P12545;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Plasminogen precursor (EC 3.4.21.7).

GN PLG.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.

OC Cercopithecoidea; Macaca.

NCBI TaxID=9544;

[1]

SEQUENCE FROM N.A.

MEDLINE=89174660; PubMed=2925643;

Tomlinson J.B., McLean J.W., Lawn R.M.,

"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis."

RL J. Biol. Chem. 264:5957-5965(1989).

CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.

CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STREPTOKINASE.

CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIFIBRIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
 CC INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN 2 CHAINS HELD
 CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
 CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 5 kringle domains.

CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
 CC EMBL: J04697; AAA36901.1; --
 CC PIR: B32863; B30848.
 CC HSSP: P00747; 1PMK.

DR DR MEROPS; S01.233; --
 DR Interpro: IPR001314; Chymotrypsin.
 DR Interpro: IPR000001; Kringle.
 DR Interpro: IPR003014; PAN.
 DR Interpro: IPR003609; Pan_app.
 DR Interpro: IPR003966; Prothrombin.
 DR Interpro: IPR001254; Ser protease_Try.
 DR Pfam: PF000051; Kringle; 5.
 DR Pfam: PF000024; PAN; 1.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Plasmin; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KW Signal.

FT SIGNAL. 1 19
 FT CHAIN 20 810 PLASMINOGEN.
 FT CHAIN 20 580 PLASMIN HEAVY CHAIN A.
 FT PEPTIDE 20 96 ACTIVATION PEPTIDE.
 FT CHAIN 97 580 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 581 810 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 103 181 KRINGLE 1.
 FT DOMAIN 164 262 KRINGLE 2.
 FT DOMAIN 275 352 KRINGLE 3.
 FT DOMAIN 377 454 KRINGLE 4.
 FT DOMAIN 481 560 KRINGLE 5.
 FT DOMAIN 581 810 SERINE PROTEASE.
 FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.

FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
 FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
 FT BINDING 136 136 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 158 158 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 172 172 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 432 432 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 134 134 FIBRIN.
 FT BINDING 136 136 FIBRIN.
 FT DISULFID 49 73 BY SIMILARITY.
 FT DISULFID 53 61 BY SIMILARITY.
 FT DISULFID 103 181 BY SIMILARITY.
 FT DISULFID 124 164 BY SIMILARITY.
 FT DISULFID 152 176 BY SIMILARITY.
 FT DISULFID 185 262 BY SIMILARITY.
 FT DISULFID 188 316 BY SIMILARITY.
 FT DISULFID 206 245 BY SIMILARITY.
 FT DISULFID 234 257 BY SIMILARITY.
 FT DISULFID 275 332 BY SIMILARITY.
 FT DISULFID 296 335 BY SIMILARITY.
 FT DISULFID 324 347 BY SIMILARITY.
 FT DISULFID 377 454 BY SIMILARITY.
 FT DISULFID 398 437 BY SIMILARITY.
 FT DISULFID 426 449 BY SIMILARITY.
 FT DISULFID 481 560 BY SIMILARITY.
 FT DISULFID 502 543 BY SIMILARITY.
 FT DISULFID 531 555 BY SIMILARITY.
 FT DISULFID 567 685 BY SIMILARITY.
 FT DISULFID 577 585 BY SIMILARITY.
 FT DISULFID 607 623 BY SIMILARITY.
 FT DISULFID 699 766 BY SIMILARITY.
 FT DISULFID 729 745 BY SIMILARITY.
 FT DISULFID 756 784 BY SIMILARITY.
 FT CARBOHYD 365 365 O-LINKED (GLYCAN. ...) (BY SIMILARITY).
 SQ SEQUENCE 810 AA; 90255 MW; A/5E1CS1A1A0F224A C6C64;

Query Match 85.0%; Score 432; DB 1; Length 810;
 Best Local Similarity 83.7%; Pred. No. 1.6e-40;
 Matches 72; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSFFIFGTNKAQLEKXNYCNPQGD 60
 DB 478 EDDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSIFETPNRAGLEKXNYCNPQGD 537

QY 61 INGPWCYTMNPRKLPDYCDIPCLASS 86
 DB 538 VGGPWCYTMNPRKLPDYCDIPCLASS 563

RESULT 3
 PLMN_HUMAN STANDARD; PRT; 810 AA.
 ID PLMN_HUMAN
 AC P00747;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiotensin].
 GN PLS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90202879; PubMed=2218848;
 RA Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;
 RT "Characterization of the gene for human plasminogen, a key proenzyme
 RL in the fibrinolytic system.";
 RL J. Biol. Chem. 265:6104-6111(1990).
 RP [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87162490; PubMed=3030813;
 RA Foregren M., Raden B., Israelsson M., Larsson K., Heden L.-O.;

RT "Molecular cloning and characterization of a full-length cDNA clone
RT for human plasminogen.";
RL FEBS Lett. 213:254-260(1987).
RN (13)
RP SEQUENCE OF 20-810.
RA Sottrup-Jensen L., Petersen T.E., Magnusson S.;
RL Submitted (JUL-1977) to the PIR data bank.
RN (14)
RP SEQUENCE OF 292-810 FROM N.A.
RA MEDLINE=85023311; PubMed=6148961;
RX Malinowski D.P., Sadler J.E., Davie E.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT human and bovine plasminogen.";
RL Biochemistry 23:4243-4250(1984).
RN (15)
RP SEQUENCE OF 20-100.
RX MEDLINE=75093329; PubMed=122932;
RA Wiman B., Wallen P.;
RT "Structural relationship between 'glutamic acid' and 'lysine' forms
RT of human plasminogen and their interaction with the NH₂-terminal
RT activation peptide as studied by affinity chromatography.";
RL Eur. J. Biochem. 50:489-494(1975).
RN (16)
RP SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810.
RA Sottrup-Jensen L., Cleaves H., Zajdel M., Petersen T.E., Magnusson S.;
RL (in) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);
RT Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,
RL Raven Press, New York (1978).
RN (17)
RP SEQUENCE OF 483-604.
RX MEDLINE=76043692; PubMed=126863;
RA Wiman B., Wallen P.;
RT "Amino-acid sequence of the cyanogen-bromide fragment from human
RT plasminogen that forms the linkage between the plasmin chains.";
RL Eur. J. Biochem. 58:539-547(1975).
RN (18)
RP SEQUENCE OF 581-810.
RX MEDLINE=77225245; PubMed=142009;
RA Wiman B.;
RT "Primary structure of the B-chain of human plasmin.";
RL Eur. J. Biochem. 76:129-137(1977).
RN (19)
RP ACTIVE SITE.
RX MEDLINE=73149248; PubMed=4694729;
RA Robbins K.C., Bernabe P., Arradon L., Summaria L.;
RT "The primary structure of human plasminogen. II. The histidine loop
RT of human plasmin: light (B) chain active center histidine sequence.";
RL J. Biol. Chem. 248:1631-1633(1973).
RN (10)
RP ACTIVE SITE.
RX MEDLINE=69234739; PubMed=4240117;
RA Groskopf W.R., Summaria L., Robbins K.C.;
RT "Studies on the active center of human plasmin. Partial amino acid
RT sequence of a peptide containing the active center serine residue.";
RL J. Biol. Chem. 244:3590-3597(1969).
RN (11)
RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RX MEDLINE=82213905; PubMed=6919539;
RA Texter M., Vail Z., Patchy L.;
RT "Structure of the omega-aminocarboxylic acid-binding sites of human
RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
RT binding of ligand by kringles 4.";
RL J. Biol. Chem. 257:7401-7406(1982).
RN (12)
RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RX MEDLINE=85054794; PubMed=6094526;
RA Vail Z., Patchy L.;
RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
RT are essential for fibrin affinity of the kringles I domain.";
RL J. Biol. Chem. 259:13690-13694(1984).
RN (13)
RP PHOSPHORYLATION SITE SER-597.
RX MEDLINE=97345939; PubMed=9201958;

RA Wang H., Proxok M., Bretthauer R.K., Castellino F.J.;
RT "Serine-578 is a major phosphorylation locus in human plasma
RT plasminogen.";
RL Biochemistry 36:8100-8106(1997).
RN (14)
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185329; PubMed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
RN (15)
RP CARBOHYDRATE-LINKAGE SITE SER-268.
RX MEDLINE=97207306; PubMed=9054441;
RA Pirte-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
RA Pizzo S.V.;
RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
RT human plasminogen 2.";
RL J. Biol. Chem. 272:7408-7411(1997).
RN (16)
RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX MEDLINE=95042728; PubMed=7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma.";
RL Cell 79:315-328(1994).
RN (17)
RP CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE=97238710; PubMed=9102221;
RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Maden J.W.,
RA Lapevich R., Nacy C.A.;
RT "A recombinant human angiostatin protein inhibits experimental primary
RT and metastatic cancer.";
RL Cancer Res. 57:1329-1334(1997).
RN (18)
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE=92031502; PubMed=1657148;
RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
RT "Crystal and molecular structure of human plasminogen kringles 4
RT refined at 1.9-A resolution.";
RL Biochemistry 30:10576-10588(1991).
RN (19)
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE=92031503; PubMed=1657149;
RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of
RT human plasminogen kringles 4.";
RL Biochemistry 30:10589-10594(1991).
RN (20)
RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RX MEDLINE=96180691; PubMed=8611560;
RA Mathews I.I., Vanderhoff-Hanover P., Castellino F.J., Tulinsky A.;
RT "Crystal structures of the recombinant kringles 1 domain of human
RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic acid.";
RL Biochemistry 35:2567-2576(1996).
RN (21)
RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
RX MEDLINE=98198034; PubMed=9521645;
RA Chang Y., Mochalkin I., McCance S.G., Cheng B., Tulinsky A.,
RA Castellino F.J.;
RT "Structure and ligand binding determinants of the recombinant kringles
RT 5 domain of human plasminogen.";
RL Biochemistry 37:3258-3271(1998).

RN [23]
 RP STRUCTURE BY NMR OF 96-184.
 RX MEDLINE=94237157; PubMed=8181475;
 RA Rejante M.R., Llinas M.,
 RT "1H-NMR assignments and secondary structure of human plasminogen
 RT kringles 1.";
 RL Eur. J. Biochem. 221:927-937(1994).
 RN [24]
 RP STRUCTURE BY NMR OF 96-184.
 RX MEDLINE=94237158; PubMed=8181476;
 RA Rejante M.R., Llinas M.,
 RT "Solution structure of the epsilon-aminohexanoic acid complex of
 RT human plasminogen kringles 1.";
 RL Eur. J. Biochem. 221:939-949(1994).
 RN [25]
 RP STRUCTURE BY NMR OF 183-354.
 RX MEDLINE=96194156; PubMed=8652577;
 RA Soehndel S., Hu C.-K., Marti D., Afzelter M., Schaller J., Llinas M.,
 RA Rickli B.E.,
 RT "Recombinant gene expression and 1H NMR characteristics of the
 RT kringles (2 + 3) supermodule: spectroscopic/functional individuality
 RT of plasminogen kringles domains.";
 RL Biochemistry 35:2357-2364(1996).
 RN [26]
 RP STRUCTURE BY NMR OF 374-461.
 RX MEDLINE=90219023; PubMed=2157850;
 RA Atkinson R.A., Williams R.J.P.,
 RT "Solution structure of the kringles 4 domain from human plasminogen by
 RT 1H nuclear magnetic resonance spectroscopy and distance geometry.";
 RL J. Mol. Biol. 212:541-552(1990).
 RN [27]
 RP VARIANTS PHE-374 AND THR-620.

Query Match 84.6%; Score 430; DB 1; Length 810;
 Best Local Similarity 82.4%; Pred. No. 2.7e-40;
 Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 BDDCMFGNGKGYGKATTTGTPCOEWAQBPBHRSTFGTNKAGLEKXNCRNPDGD 60
 DB 478 BDDCMFGNGKGYGKATTTGTPCOEWAQBPBHRSTFGTNKAGLEKXNCRNPDGD 537
 QY 61 INGPWCYTANPRKLFDCYDIPLCAS 85
 DB 538 VGSPWCYTANPRKLFDCYDIPLCAS 562

RESULT 4
 PLAN CANFA STANDARD; PRT; 333 AA.
 AC P80009;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen (EC 3.4.21.7) (Fragment).
 GN PLG.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI TaxID=9615;
 RP [1]_TaxID=9615;
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=90175323; PubMed=2626424;
 RA Schaller J., Straub C., Kaempfer U., Rickli B.E.,
 RT "Complete amino acid sequence of canine miniplasminogen.";
 RL Protein Seq. Data Anal. 2:445-450(1989).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IT WEAKENS THE WALLS OF THE
 CC GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,

CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. ACTIVATED WITH UROKINASE AND HIGH CONCENTRATIONS OF
 CC STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains at least 1 kringles domain.
 DR HSSE; P00747; SHPG.
 DR MEROPS; S01.233; -;
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringles.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser. protease_Try.
 DR Pfam; PF00051; kringles; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; kringles; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringles; Zymogen.
 FT NON_TER 1 1
 FT CHAIN 1 103 PLASMIN HEAVY CHAIN A.
 FT CHAIN 104 333 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 4 83 KRINGLE 5.
 FT DOMAIN 104 333 SERINE PROTEASE.
 FT DISULFID 4 83 BY SIMILARITY.
 FT DISULFID 25 66 BY SIMILARITY.
 FT DISULFID 54 78 BY SIMILARITY.
 FT DISULFID 90 208 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 100 108 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 130 146 BY SIMILARITY.
 FT DISULFID 222 289 BY SIMILARITY.
 FT DISULFID 252 268 BY SIMILARITY.
 FT DISULFID 279 307 BY SIMILARITY.
 FT ACT_SITE 145 145 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 188 188 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 283 283 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT SITE 152 152 STREPTOKINASE-BINDING SITE (PROBABLE).
 FT SITE 186 186 STREPTOKINASE-BINDING SITE (PROBABLE).
 FT SITE 264 264 STREPTOKINASE-BINDING SITE (PROBABLE).
 FT SITE 277 277 SITE OF SUBSTRATE SPECIFICITY (BY SIMILARITY).
 SQ SEQUENCE 333 AA; 36678 MW; C8C0271B6C6A8D4 CRC64;

Query Match 83.7%; Score 425; DB 1; Length 333;
 Best Local Similarity 84.5%; Pred. No. 3.8e-40;
 Matches 71; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 QY 3 DDDPMFGNGKGYGKATTTGTPCOEWAQBPBHRSTFGTNKAGLEKXNCRNPDGD 62
 DB 3 DDDPMFGNGKGYGKATTTGTPCOEWAQBPBHRSTFGTNKAGLEKXNCRNPDGD 62
 QY 63 GPCWCYTANPRKLFDCYDIPLCAS 86
 DB 63 GPCWCYTANPRKLFDCYDIPLCAS 86
 RESULT 5
 PLAN SHEEP STANDARD; PRT; 343 AA.

| | | | |
|-------------|--|----------------|--|
| AC | P81286; | 1988 (Rel. 37, | Created) |
| DT | 15-DEC-1998 | (Rel. 37, | Last sequence update) |
| DE | 28-FEB-2003 | (Rel. 41, | Last annotation update) |
| DE | Plasminogen | (EC 3.4.21.7) | (Fragment). |
| GN | PLG. | | |
| OS | Ovis aries (sheep). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; | | |
| OC | Bovidae; Caprinae; Ovis. | | |
| OX | NCBI_TaxID=9940; | | |
| RN | [1] | | |
| RP | SEQUENCE. | | |
| RX | MEDLINE=9314995; PubMed=1492092; | | |
| RT | Schaller J., Straub C., Kampfer U., Rickli E.B.; | | |
| RL | "Complete amino acid sequence of ovine miniplasminogen." | | |
| CC | Protein Seq. Data Anal. 5:21-25(1992). | | |
| CC | -1 FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION: IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND VON WILLEBRAND FACTOR. | | |
| CC | -1 CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products. | | |
| CC | -1 ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STEPTOKINASE. | | |
| CC | -1 MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT. | | |
| CC | -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY. | | |
| CC | -1 SIMILARITY: Contains at least 2 kringle domains. | | |
| DR | HSSP; P00747; SHPG. | | |
| DR | MEROPS; S01.233; -. | | |
| DR | InterPro; IPR001314; Chymotrypsin. | | |
| DR | InterPro; IPR000001; Kringle. | | |
| DR | InterPro; IPR003966; Prothrombin. | | |
| DR | InterPro; IPR001254; Ser-protease_Try. | | |
| DR | Pfam; PF00051; kringle_1. | | |
| DR | Pfam; PF00089; trypsin_1. | | |
| DR | PRINTS; PR00722; CHYMOTRYPSIN. | | |
| DR | PRINTS; PR00018; KRINGLE. | | |
| DR | PRINTS; PR01505; PROTHROMBIN. | | |
| DR | ProDom; PD000395; Kringle_1. | | |
| DR | SMART; SM00130; KR_1. | | |
| DR | SMART; SM00020; Tryp_Spc_1. | | |
| DR | PROSITE; PS00021; KRINGLE_1; 1. | | |
| DR | PROSITE; PS00070; KRINGLE_2; 1. | | |
| DR | PROSITE; PS00240; TRYPSIN_DOM; 1. | | |
| DR | PROSITE; PS00134; TRYPSIN_HIS; 1. | | |
| DR | PROSITE; PS00135; TRYPSIN_SER; 1. | | |
| KW | Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis; | | |
| KW | Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat. | | |
| FT | NON_TER | 1 | |
| FT | DOMAIN | <1 | 140 HEAVY CHAIN A. |
| FT | DOMAIN | 141 | >343 LIGHT CHAIN A. |
| FT | DOMAIN | <1 | 17 KRINGLE 4. |
| FT | DOMAIN | 41 | 120 KRINGLE 5. |
| FT | DOMAIN | 114 | 341 SERINE PROTEASE. |
| FT | ACT_SITE | 181 | 181 SERINE RELAY SYSTEM. |
| FT | ACT_SITE | 224 | 224 CHARGE RELAY SYSTEM. |
| FT | ACT_SITE | 319 | 319 CHARGE RELAY SYSTEM. |
| FT | NON_TER | 343 | 343 |
| SO | SEQUENCE | 343 AA; | 8DF6EBA92D596EE0 CRC64; |
| Query Match | | 81.9%; | Score 416; DB 1; Length 343; |
| Similarity | | 82.6%; | Pred. NO. 4e-39; 14; Indels 0; Gaps 0; |
| Matches | 71; Conservative | 1; | Mismatches 0; Gaps 0; |

| | | | |
|-----------|--|--|------------------------|
| Oy | I | EDOCBENGNGVGRKATATWTGCPCEMAAOEPHRSTFIPGNWKAGLEKXNCNPDD | 6 |
| Db | 12 | EADDMGIGGVGRKATTVAGVPCCEMAAOEPHRGIFTPTNPRAGLEKXNCNPDD | 71 |
| Oy | 61 | INGFWCTYNNPRKLPDYCDIPLCASS | 86 |
| Db | 72 | VNGPWCTTNPRLFPDYCDIPCESS | 97 |
| RESULT 6 | | | |
| PLN_HORSE | STANDARD; | PTI; | 338 AA. |
| ID | PLN_HORSE | STANDARD; | PTI; 338 AA. |
| AC | P80010; | | |
| DT | 01-NOV-1991 (Rel. 20, Created) | | |
| DT | 01-NOV-1991 (Rel. 20, Last sequence update) | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | |
| DE | Plasminogen (EC 3.4.21.7) (Fragment). | | |
| GN | PLG. | | |
| OS | Equus caballus (Horse). | | |
| OC | Bufo vulgaris (Toad); Chiroptera; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Perissodactyla; Equidae; Equus. | | |
| OX | NCBI_TaxID=9796; | | |
| RN | [1] | | |
| RP | SEQUENCE. | | |
| RC | TISSUE=Plasma; | | |
| RA | MEDLINE=92052077; PubMed=1946332; | | |
| RA | Schaller J., Straub C., Kaempfer U., Rickli B.E.; | | |
| RT | "Complete amino acid sequence of equine multiplasminogen."; | | |
| RL | Protein Seq. Data Anal. 4:69-74(1991). | | |
| CC | -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS | | |
| CC | A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING | | |
| CC | EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, | | |
| CC | AND INFLAMMATION; IT INACTIVATES THE WALS OF THE | | |
| CC | GAAIPAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN | | |
| CC | ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH | | |
| CC | AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, | | |
| CC | LAMININ AND VON WILLEBRAND FACTOR. | | |
| CC | -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys- -Xaa > Arg- -Xaa; | | |
| CC | higher selectivity than trypsin. Converts fibrin into soluble | | |
| CC | products. | | |
| CC | -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN | | |
| CC | ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO | | |
| CC | FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STEPTOKINASE. | | |
| CC | -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN | | |
| CC | IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT. | | |
| CC | -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY. | | |
| CC | -1- SIMILARITY: Contains at least 1 kringle domain. | | |
| DR | PIR: A61545; A61545. | | |
| DR | HSSP; P00747; SHRP. | | |
| DR | MEROPE; S01.233; -. | | |
| DR | InterPro: IPR001314; Chymotrypsin. | | |
| DR | InterPro: IPR000001; Kringle. | | |
| DR | InterPro: IPR003966; Prothrombin. | | |
| DR | InterPro: IPR001254; Ser.protease_Try. | | |
| DR | Pfam; PF00085; kringle_1. | | |
| DR | Pfam; PF00089; trypsin_1. | | |
| DR | PRINTS; PR00722; CHYMOTRYPSIN. | | |
| DR | PRINTS; PR00018; KRINGLE. | | |
| DR | PRINTS; PR01505; PROTHROMBIN. | | |
| DR | ProDom; PD000395; Kringle; 1. | | |
| DR | SMART; SM00130; KR; 1. | | |
| DR | SMART; SM00020; Tryp_Spc; 1. | | |
| DR | PROSITE; PS00021; KRINGLE_1; 1. | | |
| DR | PROSITE; PS00070; KRINGLE_2; 1. | | |
| DR | PROSITE; PS02040; TRYPSIN_DOM; 1. | | |
| DR | PROSITE; PS00134; TRYPSIN_HIS; 1. | | |
| DR | PROSITE; PS00135; TRYPSIN_SER; 1. | | |
| KW | Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis; | | |
| KW | Tissue remodeling; Blood coagulation; Kringle; Zymogen. | | |
| FT | NON TER | 1 | |
| FT | CHAIN | <1 | 108 |
| FT | CHAIN | 109 | 338 |
| FT | DOMAIN | 9 | 88 |
| | | | PLASMIN HEAVY CHAIN A. |
| | | | PLASMIN LIGHT CHAIN B. |
| | | | KRINGLE 5. |

DR InterPro: IPR000001; Kringle-
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003509; Pan app.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00051; Kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PRO0018; KRINGLE.
 DR PRINTS: PRO1505; PROTHROMBIN.
 DR PRODOM: PD000395; Kringle; 5.
 DR SMART: SM00130; KR; 5.
 DR SMART: SM00473; PAN AP; 1.
 DR SMART: SM00020; TRY_Spc; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS50070; KRINGLE_2; 5.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KW Signal.
 FT CHAIN 1 19 PLASMINOGEN.
 FT CHAIN 20 812 PLASMIN HEAVY CHAIN A.
 FT CHAIN 20 581 ACTIVATION PEPTIDE.
 FT PEPTIDE 20 97 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 98 581 ANGIOTATIN.
 FT CHAIN 98 7436 PLASMIN LIGHT CHAIN B.
 FT CHAIN 582 812 KRINGLE 1.
 FT DOMAIN 103 181 KRINGLE 2.
 FT DOMAIN 184 262 KRINGLE 3.
 FT DOMAIN 275 352 KRINGLE 4.
 FT DOMAIN 377 454 KRINGLE 5.
 FT DOMAIN 481 560 SERINE PROTEASE.
 FT DOMAIN 582 812 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 624 624 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 667 667 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 49 73 BY SIMILARITY.
 FT DISULFID 53 61 BY SIMILARITY.
 FT DISULFID 103 181 BY SIMILARITY.
 FT DISULFID 124 164 BY SIMILARITY.
 FT DISULFID 152 176 BY SIMILARITY.
 FT DISULFID 185 262 BY SIMILARITY.
 FT DISULFID 188 316 BY SIMILARITY.
 FT DISULFID 206 245 BY SIMILARITY.
 FT DISULFID 234 257 BY SIMILARITY.
 FT DISULFID 275 352 BY SIMILARITY.
 FT DISULFID 296 335 BY SIMILARITY.
 FT DISULFID 324 347 BY SIMILARITY.
 FT DISULFID 377 454 BY SIMILARITY.
 FT DISULFID 398 437 BY SIMILARITY.
 FT DISULFID 426 449 BY SIMILARITY.
 FT DISULFID 481 560 BY SIMILARITY.
 FT DISULFID 502 543 BY SIMILARITY.
 FT DISULFID 531 555 BY SIMILARITY.
 FT DISULFID 568 687 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 578 586 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 609 625 BY SIMILARITY.
 FT DISULFID 701 768 BY SIMILARITY.
 FT DISULFID 731 747 BY SIMILARITY.
 FT DISULFID 758 786 BY SIMILARITY.
 FT CONFLICT 235 235 R -> H (IN REF. 1).
 FT CONFLICT 235 235 G -> D (IN REF. 1).
 FT CONFLICT 525 525 S -> L (IN REF. 1).
 FT CONFLICT 649 649 S -> L (IN REF. 1).
 SQ SEQUENCE 812 AA; 90781 MW; 241732606A2FFD2 CRC64;

Query Match 81.3%; Score 413; DB 1; Length 812;
 Best Local Similarity 80.2%; Pred. No. 2.1e-38;
 Matches 69; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
 1 EDDCMFGNGKGYGKATVVTGTPCGMAOEPHHSFTIPGINKMAGLEKNYCRNPDGD 60

DB 478 EDDCMFGNGKDYGKATVTAAGTPCGMAOEPHHSFTIPGINKMAGLEKNYCRNPDGD 537
 QY 61 INGPWCYTNNPRKLPDYCDIPICASS 86
 DB 538 VNGPCYTNNPRKLPDYCDIPICASS 563
 RESULT 8
 PLAN_PIG
 ID PLAN_PIG STANDARD; PRT; 790 AA.
 AC P06867;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen (BC 3.4.21.7).
 GN PLG.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE OF 1-560.
 RA Schaller J., Marti T., Roesselet S.J., Kaempfer U., Rickli E.E.;
 RT "Amino acid sequence of the heavy chain of porcine plasmin. Comparison
 of the carbohydrate attachment sites with the human and bovine
 species.";
 RL Fibrinolysis 1:91-102(1987).
 RN [2]
 RP SEQUENCE OF 450-790.
 RA MEDLINE=85203907; PubMed=3846533;
 RA Marti T., Schaller J., Rickli E.E.;
 RT "Determination of the complete amino-acid sequence of porcine
 miniplasminogen.";
 RL Eur. J. Biochem. 149:279-285(1985).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 plasminogen. Species specificity in relation to stalylation and
 fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa -> Arg-|-Xaa;
 higher selectivity than trypsin. Converts fibrin into soluble
 products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PTM: N-LINKED GLYCAN CONTAINS N-ACETYLGLUCOSAMINE, SIALIC ACID AND
 IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAc
 DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
 (MICROHETEROGENEITY).
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 DR HSSP; P03733; PLPG.
 DR PIR; S00747; SHPG.
 DR MEROPS; S01.233; -;
 DR GlycoSuiteDB; P06867; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.

DR InterPro; IPR003609; Pan. app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser. protease_Try.
 DR Pfam; PF00051; kringleg; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringleg; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN AP; 1.
 DR SMART; SM00020; TRYP SPc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_SER; 1.
 DR PROSITE; PS00135; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_HIS; 1.
 DR Tissue remodeling; Blood coagulation; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Plasma; Glycoprotein; Fibrinolysis;
 FT CHAIN 1 560 PLASMIN HEAVY CHAIN A.
 FT CHAIN 561 790 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 561 790 SERINE PROTEASE.
 FT DOMAIN 162 162 KRINGLE 1.
 FT DOMAIN 166 243 KRINGLE 2.
 FT DOMAIN 256 333 KRINGLE 3.
 FT DOMAIN 358 435 KRINGLE 4.
 FT DOMAIN 461 540 KRINGLE 5.
 FT ACT SITE 602 602 CHARGE RELAY SYSTEM.
 FT ACT SITE 645 645 CHARGE RELAY SYSTEM.
 FT ACT SITE 740 740 CHARGE RELAY SYSTEM.
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 340 340 /FTID-CAR 000019.
 FT CARBOHYD 340 340 O-LINKED (GALNAC. . .).
 FT SEQUENCE 790 AA; 88592 MW; F04EA06E74BCD58E CRC64;
 SQ
 Query Match 80.5%; Score 409; DB 1; Length 790;
 Best Local Similarity 80.0%; Pred. No. 5.7e-38;
 Matches 68; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 QY 2 ODCMPGNGKGYRGRKATVTVTPCQEMAAQEPHRSFTPGTNKAGLEKRYCRNPDGDI 61
 DB 459 EDCMPGNGKRYRGRKATVTVTPCQEMAAQEPHRSFTPGTNKAGLEKRYCRNPDGDI 518
 QY 62 NGPWCTTNPRLKFDYCDIPLCASS 86
 DB 519 NGPWCTTNPRLKFDYCDIPLCASS 543
 RESULT 9
 PLMN BOVIN STANDARD; PRT; 812 AA.
 ID PLMN BOVIN Q28162;
 AC P06868; Q28162;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasmogen precursor (EC 3.4.21.7).
 GN PLG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxId=9913;
 OK NCBI_TaxId=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Berglund L., Andersen M.D., Petersen T.E.;
 RT "Cloning and characterization of the bovine plasminogen cDNA.";
 RL Int. Dairy J. 5:593-603(1995).
 RN (2)
 RP SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=85203906; PubMed=3846532;

RA Schaller J., Moser P.W., Dammeger-Muller G.A.K., Rosselet S.J.,
 RA Kamper U., Rickli E.B.;
 RT "Complete amino acid sequence of bovine plasminogen. Comparison with
 RT human plasminogen.";
 RL Eur. J. Biochem. 149:267-278(1985).
 RN (3)
 RP SEQUENCE OF 706-812 FROM N.A.
 RX MEDLINE=85023311; PubMed=6148961;
 RA Malinowski D.P., Sadler J.E., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 RT human and bovine plasminogen.";
 RL Biochemistry 23:4243-4250(1984).
 RN (4)
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Mari T., Schaller J., Rickli E.B., Schmid K., Kameiling J.P.,
 RA Gervig G.U., van Halbeek H., Vliegenhart J.F.;
 RT The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to stialation and
 RT fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PTM: N-LINKED GLYCANS CONTAIN N-ACETYLGLUCOSAMINE AND SIALIC ACID.
 CC O-LINKED GLYCANS CONSIST OF GAL-GALNAC DISACCHARIDE WITH IS
 CC MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 5 kringleg domains.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X79402; CAA55939.1; -;
 DR EMBL; K02935; AAA0714.1; -;
 DR PIR; S45046; PLBO.
 DR HSRP; P00747; 2PK4.
 DR MEROPS; S01.233; -;
 DR GlycoSuiteDB; P06868; -;
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringleg.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser. protease_Try.
 DR Pfam; PF00051; Kringleg; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringleg; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN AP; 1.
 DR SMART; SM00020; TRYP_Spc; 1.

DR PROSITE; PS00021; KRINGLE 1; 5.
 DR PROSITE; PS00070; KRINGLE 2; 5.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KW Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 812 PLASMINOGEN.
 FT CHAIN 27 583 PLASMIN HEAVY CHAIN A.
 FT CHAIN 584 812 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 110 188 KRINGLE 1.
 FT DOMAIN 192 269 KRINGLE 2.
 FT DOMAIN 282 359 KRINGLE 3.
 FT DOMAIN 384 461 KRINGLE 4.
 FT DOMAIN 485 564 KRINGLE 5.
 FT DOMAIN 584 812 SERINE PROTEASE.
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 315 315 /FTID-CAR 000014.
 FT CARBOHYD 365 365 /FTID-CAR 000015.
 FT ACT SITE 624 624 CHARGE RELAY SYSTEM.
 FT ACT SITE 667 667 CHARGE RELAY SYSTEM.
 FT ACT SITE 762 762 CHARGE RELAY SYSTEM.
 FT CONFLICT 335 335 N -> D (IN REF. 2).
 FT CONFLICT 516 516 O -> H (IN REF. 2).
 FT CONFLICT 555 555 P -> L (IN REF. 2).
 FT CONFLICT 744 744 T -> R (IN REF. 3).
 FT SEQUENCE 812 AA; 91216 MW; 3846AA691E220946 CRC64;
 SQ
 Query Match 79.9%; Score 406; DB 1; Length 812;
 Best Local Similarity 77.9%; Pred. No. 1,3e-37;
 Matches 67; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
 QY 1 EODCMGNGKGYRGKATVTGTPCEMAAQBHRHSTFPGTNKAGLEKNTCRNPDGD 60
 DB 482 EADCMGIGTSYRGKATVTAGVPCQMAAQBHRHSTFPGTNKAGLEKNTCRNPDGD 541
 QY 61 INGPWCYTNNPKLFYCDPLFCASS 86
 DB 542 VNGPWCYTNNPKRFYCDVPCDCESS 567
 RESULT 10
 ID PLAN_ERIEU STANDARD; PRT; 810 AA.
 AC Q29485;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7).
 GN PUG.
 OS Etrineaus europaeus (Western European hedgehog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eultheria; Insectivora; Erinaceidae; Erinaceus.
 OK NCBI_TaxID=9365;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96025778; PubMed=7592597;
 RA Lawn R.M., Boomark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
 RA Byrne C.D., Pong K.J., Meer K., Patchy L.,
 RT "The recurring evolution of lipoprotein(a). Insights from cloning of
 RT hedgehog apolipoprotein(a)."
 RT J. Biol. Chem. 270:24004-24009 (1995).
 RL [2]
 RP REVISIONS.
 RA Lawn R.M.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,

CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa -> Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE
 CC -!- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -!- SIMILARITY: Contains 5 kringle domains.
 CC -----
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 CC -----
 CC EMBL; U33171; AAC48717.1; -.
 CC PIR; I46260; I46260.
 CC HSSP; P00747; 1PMK.
 CC MEROPS; S01.233; -.
 CC InterPro; IPR001314; Chymotrypsin.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR003609; Pan. app.
 CC InterPro; IPR003609; Pan. app.
 CC InterPro; IPR003966; Prothrombin.
 CC InterPro; IPR001254; Ser. protease_Try.
 CC Pfam; PR00051; kringle; 5.
 CC Pfam; PR00024; PAN; 1.
 CC Pfam; PR00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00018; KRINGLE.
 CC PRINTS; PR01505; PROTHROMBIN.
 CC PRODOM; PD000395; Kringle; 5.
 CC SMART; SM00130; KR; 5.
 CC SMART; SM00473; PAN_AP; 1.
 CC SMART; SM00020; TRY_SPC; 1.
 CC PROSITE; PS00021; KRINGLE 1; 5.
 CC PROSITE; PS00070; KRINGLE 2; 5.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KW Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 810 PLASMINOGEN.
 FT CHAIN 20 582 PLASMIN HEAVY CHAIN A (BY SIMILARITY).
 FT CHAIN 583 810 PLASMIN LIGHT CHAIN B (BY SIMILARITY).
 FT DOMAIN 103 181 SERINE PROTEASE.
 FT DOMAIN 185 262 KRINGLE 1.
 FT DOMAIN 275 352 KRINGLE 2.
 FT DOMAIN 379 456 KRINGLE 3.
 FT DOMAIN 482 561 KRINGLE 4.
 FT DOMAIN 582 662 KRINGLE 5.
 FT ACT SITE 622 622 CHARGE RELAY SYSTEM.
 FT ACT SITE 665 665 CHARGE RELAY SYSTEM.
 FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 810 AA; 90902 MW; 8E75780946017A16 CRC64;
 Query Match 76.4%; Score 388; DB 1; Length 810;
 Best Local Similarity 77.6%; Pred. No. 1,3e-35;
 Matches 66; Conservative 3; Mismatches 16; Indels 0; Gaps 0;
 QY 1 EODCMGNGKGYRGKATVTGTPCEMAAQBHRHSTFPGTNKAGLEKNTCRNPDGD 60

DB 479 EDCIIDNGKGYGTATGATGATCCAMAAQEPHRSIFETPETNPRADLOENYCRNPDGD 538
QY 61 INGPWCYTMNPRKLPYCDIPLCAS 85
DB 539 ANGPWCYTMNPRKLPYCDIPHCVS 563

RESULT 11
PLMN RAT
ID PLMN RAT STANDARD; PRT; 169 AA.
AC 001177;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN Plg.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91250378; PubMed=1645711;
RA Kanakas J.J., Makker S.P.;
RT Identification of the rat Heymann nephritis autoantigen (GP330) as a
RT receptor site for plasminogen.";
RL J. Biol. Chem. 266:10825-10829(1991).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION: IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 5 kringle domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M62832; AAA1884.1; -.
DR F1R; A40522; A40522.
DR HSSP; P00747; 1PMK.
DR MEROPS; S01.233; -.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser. protease_Try.
DR Pfam; PF00051; Kringle_2.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle_2.
DR SMART; SM00130; KR_1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS02040; TRYPSIN_DOM; PARTIAL.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.

KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Repeat.
FT NON TER 1
FT DOMAIN <1 10 KRINGLE 3 (BY SIMILARITY).
FT DOMAIN 34 112 KRINGLE 4 (BY SIMILARITY).
FT DOMAIN 139 >169 KRINGLE 5 (BY SIMILARITY).
FT DISULFID 34 112 BY SIMILARITY.
FT DISULFID 55 95 BY SIMILARITY.
FT DISULFID 83 107 BY SIMILARITY.
FT NON TER 169
SQ SEQUENCE 169 AA; 18401 MW; 77A54214C9D010C CRC64;
Query Match 47.9%; Score 243.5; DB 1; Length 169;
Best Local Similarity 48.2%; Pred. No. 3.3e-20;
Matches 41; Conservative 12; Mismatches 31; Indels 1; Gaps 1;
QY 2 QDCMFGNGKGYRGKATVTGTPCEMAAQBPHRSITFGINKAGIEKRYCRPPDGI 61
DB 32 QECYGNKSKYRGTSTNTGKCKQSWMTPHSHK-TPANFPDSDGEMNYCRNPDMDQ 90
QY 62 NGPWCYTMNPRKLPYCDIPLCAS 86
DB 91 RGPWCFTTDPSTVRYWYCNLKRCSER 115

RESULT 12
HGFL HUMAN
ID HGFL HUMAN STANDARD; PRT; 711 AA.
AC P26227; Q13350; Q14870;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
DE stimulatory protein) (MSP) (Macrophage stimulating protein).
GN MSL1 OR HGFL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92002016; PubMed=1655021;
RA Han S., Stuart L.A., Fritzen Degen S.J.;
RT Characterization of the DNPISS2 locus on human chromosome 3;
RT identification of a gene coding for four kringle domains with
RT homology to hepatocyte growth factor.";
RL Biochemistry 30:9768-9780(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93340141; PubMed=8393443;
RA Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
RT Cloning, sequencing, and expression of human macrophage stimulating
RT protein (MSP, MSL1) confirms MSP as a member of the family of Kringle
RT proteins and locates the MSP gene on chromosome 3.";
RL J. Biol. Chem. 268:15461-15468(1993).
CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
CC CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
CC CONSERVED.
CC -1- PTM: MAY BE CLEAVED AFTER AA 484, TO YIELD A TWO-CHAIN MOLECULE
CC HELD TOGETHER BY DISULFIDE BONDS, OR TWO SEPARATE POLYPEPTIDES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: Contains 4 kringle domains.
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DR EMBL; M74178; AAA50165.1; -
 DR EMBL; U37055; AAC50472.1; -
 DR EMBL; L11924; AAA59872.1; -
 DR PIR; A40331; A47136.
 DR HSSP; P00747; 2PK4.
 DR MEROPS; S01.975; -
 DR Genew; HGNC; 7380; MST1.
 DR MIM; 142408; -
 DR InterPro; IPR003314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser.protease_Try.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR PRODOM; PD000395; Kringle; 4.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS50070; KRINGLE_2; 4.
 DR PROSITE; PS50240; TRYPsin_Dom; 1.
 DR Kinsase; Glycoprotein; Serine protease homolog; Repeat; Signal;
 KM Polymorphism.
 FT SIGNLV 1 18 POTENTIAL.
 FT CHAIN 19 711 HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.
 FT DOMAIN 32 109 PAP.
 FT DOMAIN 110 186 KRINGLE 1.
 FT DOMAIN 191 268 KRINGLE 2.
 FT DOMAIN 283 361 KRINGLE 3.
 FT DOMAIN 370 448 KRINGLE 4.
 FT DOMAIN 484 711 SERINE PROTEASE-LIKE.
 FT DISULFID 56 78 BY SIMILARITY.
 FT DISULFID 60 66 BY SIMILARITY.
 FT DISULFID 110 186 BY SIMILARITY.
 FT DISULFID 131 169 BY SIMILARITY.
 FT DISULFID 157 181 BY SIMILARITY.
 FT DISULFID 191 268 BY SIMILARITY.
 FT DISULFID 194 324 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 212 251 BY SIMILARITY.
 FT DISULFID 240 263 BY SIMILARITY.
 FT DISULFID 283 361 BY SIMILARITY.
 FT DISULFID 304 343 BY SIMILARITY.
 FT DISULFID 332 355 BY SIMILARITY.
 FT DISULFID 370 448 BY SIMILARITY.
 FT DISULFID 391 431 BY SIMILARITY.
 FT DISULFID 419 443 BY SIMILARITY.
 FT DISULFID 468 588 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 507 523 BY SIMILARITY.
 FT DISULFID 602 667 BY SIMILARITY.
 FT DISULFID 632 646 BY SIMILARITY.
 FT DISULFID 657 685 BY SIMILARITY.
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 13 13 Y -> C.
 FT VARIANT 212 212 /FTID=VAR_006631.
 FT VARIANT 212 212 C -> F.
 FT VARIANT 676 676 /FTID=VAR_006632.
 FT VARIANT 676 676 E -> K (IN dSNP: 7798).
 FT CONFLICT 623 623 /FTID=VAR_014569.
 FT CONFLICT 623 623 L -> F (IN REF. 2).
 FT SEQUENCE 711 AA; 80379 MW; 596ED21F180290E4 CRC64;
 Query Match 47.5%; Score 241.5; DB 1; Length 711;
 Best Local Similarity 51.8%; Pred. No. 2.5e-19;
 Matches 43; Conservative 11; Mismatches 28; Indels 1; Gaps 1;

QY 2 ODCMFGNGKGYRKATVYTGPCQEWAAQEPHRHSTFPGTNKAGLEKNTCRNPDGI 61
 Db 368 QDCYHAGGEQYGVTSKTRKGVQCCQWMSAETPHK-PQFETSEPHQLEHNCRNPDGS 426
 QY 62 NGPWCYTNAPRKLPYCDIPLCA 84
 Db 427 HGPWCYTMDBRTPFDYCALRCA 449
 RESULT 13
 HGFL MOUSE
 ID HGFL_MOUSE STANDARD; PRT; 716 AA.
 AC P26928;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hepatocyte growth factor-like protein precursor (Macrophage
 stimulatory protein) (MSP).
 GN MST1 OR HGFL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=92002017; PubMed=1832957;
 RA Friesner Degen S.J., Stuart L.A., Han S., Jamison C.S.;
 RT "Characterization of the mouse cdna and gene coding for a hepatocyte
 growth factor-like protein: expression during development.";
 RL Biochemistry 30:9781-9791(1991).
 CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
 CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
 CONSERVED
 CC -1- TISSUE SPECIFICITY: LIVER. LOWER LEVELS IN LUNG, PLACENTA AND
 ADRENAL.
 CC -1- DEVELOPMENTAL STAGE: IS EXPRESSED AT LOW LEVELS DURING GESTATION.
 CC JUST BEFORE BIRTH THE LEVEL INCREASES DRAMATICALLY AND REMAINS
 STABLE AFTERWARDS.
 CC -1- PTM: MAY BE CLEAVED AFTER AA 488, TO YIELD A TWO-CHAIN MOLECULE
 HELD TOGETHER BY DISULFIDE BONDS, OR CLEAVED INTO TWO SEPARATE
 POLYPEPTIDES.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 4 kringle domains.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M74180; AAA50166.1; -
 DR EMBL; M74181; AAA50167.1; -
 DR PIR; A40332; A40332.
 DR HSSP; P00747; 1XRN.
 DR MEROPS; S01.975; -
 DR MCD; MGI; 96080; Mcl1.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser.protease_Try.
 DR Pfam; PF00051; kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR PRODOM; PD000395; Kringle; 4.
 DR SMART; SM00130; KR; 4.

DR SMART; SMO0473; PAN AP; 1.
DR SMART; SMO0020; TRYD SPEC; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS50070; KRINGLE_2; 4.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW Kringle; Glycoprotein; Serine protease homolog; Repeat; Signal.
FT SIGNAL 1 18
FT CHAIN 19 716
FT DOMAIN 19 109
FT DOMAIN 110 186
FT DOMAIN 191 268
FT DOMAIN 292 370
FT DOMAIN 379 457
FT DOMAIN 489 716
FT DISULFID 56 78
FT DISULFID 60 66
FT DISULFID 110 186
FT DISULFID 131 169
FT DISULFID 157 181
FT DISULFID 191 268
FT DISULFID 194 333
FT DISULFID 212 251
FT DISULFID 240 263
FT DISULFID 292 370
FT DISULFID 313 352
FT DISULFID 341 364
FT DISULFID 379 457
FT DISULFID 400 440
FT DISULFID 428 452
FT DISULFID 477 593
FT DISULFID 512 528
FT DISULFID 607 672
FT DISULFID 637 651
FT DISULFID 662 690
FT CARBOHYD 72 72
FT CARBOHYD 173 173
FT CARBOHYD 305 305
FT CARBOHYD 620 620
FT CONFLICT 19 19
SQ SEQUENCE 716 AA; 80588 MW; BACE02EF85213ACC CRC64;
Query Match 47.1%; Score 239.5; DB 1; Length 716;
Best Local Similarity 48.8%; Pred. No. 4.2e-19;
Matches 40; Conservative 14; Mismatches 27; Indels 1; Gaps 1
Db 2 ODCMFGNGKGRGKATVGTGTCCEMAOEHRSSTFGTNKAGLEKRYCRAPDGI 61
377 EGCYHSGSEQYRGSVKTRKGVQCCHMSSEFTHK-PTPTPSAPQAGLEAFNCRAPDDDS 435
QY 62 NGPMCYTNPRKLPDYCDIPLC 83
Db 436 HGPWCYTLDPDILFDYCALORC 457
RESULT 14
APOA_MACMU STANDARD; PRT; 1420 AA.
ID APOA_MACMU
AC P14417;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE APO1ipoprotein(a) (BC 3.4.21.-) (Apo(a)) (4p(a)) (Fragment).
GN Lp(a).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCB1_TaxID=9544;
OX 1
RN 1
SEQUENCE FROM N.A.
RP MEDLINE=89174660; PubMed=2925643;
RA Tomlinson J.E., McLean J.W., Lawn R.M.;
RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of

```

RT      syntheis,":
J. Biol. Chem. 264:5957-5965(1989).
-1- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
      (lp(a)). It has serine proteinase activity and is able of
      autolysis, inhibits tissue-type plasminogen activator 1.
      lp(a) may be a ligand for megalin/cp 330.
-1- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
      decorin (By similarity).
-1- PTM: N- and O-glycosylated (By similarity).
-1- DISEASE: Elevated plasma concentrations of apo(a) and its
      naturally occurring proteolytic fragments are correlated with
      atherosclerosis. Homology with plasminogen kringle IV and V is
      thought to underlie the atherogenicity of the protein, because the
      fragments are competing with plasminogen for fibrinogen binding.
-1- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
      leading to the formation of the so called mini-lp(a). Apo(a)
      fragments accumulate in atherosclerotic lesions, where they may
      promote thrombogenesis. O-glycosylation may limit the extent of
      proteolytic fragmentation (By similarity).
-1- SIMILARITY: BELONGS TO PERTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
-1- SIMILARITY: Contains at least 10 kringle domains.
CC      CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      entities requires a license agreement (See http://www.1db-sib.ch/announce/).
CC      or send an email to license@1db-sib.ch).
CC      CC
CC      EMBL: J04635; AAA36833.1; -.
DR      PIR: A32869; A32869.
DR      HSSP: P00747; 2PK4.
DR      MEROPS: S01.226; -.
DR      InterPro: IPR001314; Chymotrypsin.
DR      InterPro: IPR000001; Kringle.
DR      InterPro: IPR001254; Ser_Protease_Try.
DR      Pfam: PF00051; Kringle; 11.
DR      Pfam: PF00089; trypsin; 1.
DR      PRINTS: PR00722; CHYMOTRYPSIN.
DR      PRINTS: PR00018; KRINGLE.
DR      ProDom: PD000395; Kringle; 10.
DR      SMART: SM00130; KR; 10
DR      SMART: SM00020; TRY_P_Spc; 1.
DR      PROSITE: PS00021; KRINGLE_1; 10.
DR      PROSITE: PS00070; KRINGLE_2; 10.
DR      PROSITE: PS02040; TRYPsin_DOM; 1.
DR      PROSITE: PS00134; TRYPsin_HIS; FALSE_NEG.
DR      PROSITE: PS00135; TRYPsin_SER; FALSE_NEG.
KW      Hydroxylase, Serine protease; Lipid transport; Plasma; Glycoprotein;
      Kringle; Repeat; Atherosclerosis.
FT      NON TER          1          1
FT      DOMAIN           49      127      KRINGLE 1.
FT      DOMAIN           163      241      KRINGLE 2.
FT      DOMAIN           277      355      KRINGLE 3.
FT      DOMAIN           391      469      KRINGLE 4.
FT      DOMAIN           505      583      KRINGLE 5.
FT      DOMAIN           619      697      KRINGLE 6.
FT      DOMAIN           725      803      KRINGLE 7.
FT      DOMAIN           839      917      KRINGLE 8.
FT      DOMAIN           953      1031     KRINGLE 9.
FT      DOMAIN           1067      1145     KRINGLE 10.
FT      DOMAIN           1191      1420     SERINE PROTEASE.
SQ      SEQUENCE        1420 AA; 158367 MW; BE102949E03C5B0E CRC64;
Query Match          46.5%; Score 236; DB 1; Length 1420;
Best Local Similarity 49.4%; Pred. No. 2,le-16;
Matches 42; Conservative 12; Mismatches 23; Indels 8; Gaps 3;
Oy      2 QDCMFGKGVKGVKATVTGTGTCQEWAAQEPHRHS---TFIPGTNWKAGLEKRYCNPD 58
Db      QDCMFGKGVKGVKATVTGTGTCQEWAAQEPHRHS---TFIPGTNWKAGLEKRYCNPD 58
      724 QDCMFGKGVKGVKATVTGTGTCQEWAAQEPHRHS---TFIPGTNWKAGLEKRYCNPD 729

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QY 59 GDINGPWCYTMNPKLFDCDPLC 83
 Db 780 AEIR-PWCYTMNPKLFDCDPLC 803

RESULT 15
 HGF_HUMAN STANDARD; PRT; 728 AA.
 AC P14210; O98YL9; O9UDU6;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hepatocyte growth factor precursor (Scatter factor) (SF)
 DE (Hepatopoietin A).
 GN HGF OR HPTA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=91340155; PubMed=1831432;
 RA Seki T., Hagiya M., Shimomishi M., Nakamura T., Shimizu S.;
 RT "Organization of the human hepatocyte growth factor-encoding gene.";
 RL Gene 102:213-219 (1991).
 [2]
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=9932017; PubMed=2528952;
 RA Miyazawa K., Teubouch H., Naka D., Takahashi K., Okigaki M.,
 RA Arakaki N., Nakayama H., Hirono S., Sakiyama O., Takahashi K.,
 RA Gohda E., Daikuhara Y., Kitamura N.;
 RT "Molecular cloning and sequence analysis of cDNA for human hepatocyte
 growth factor.";
 RL Biochem. Biophys. Res. Commun. 163:967-973 (1989).
 [3]
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=91025062; PubMed=2145836;
 RA Seki T., Ihara I., Sugimura A., Shimomishi M., Nishizawa T.,
 RA Aami O., Hagiya M., Nakamura T., Shimizu S.;
 RT "Isolation and expression of cDNA for different forms of hepatocyte
 growth factor from human leukocyte.";
 RL Biochem. Biophys. Res. Commun. 172:321-327 (1990).
 [4]
 RN RP SEQUENCE FROM N.A. AND SEQUENCE OF 55-73 AND 495-520.
 RX MEDLINE=9006676; PubMed=2531289;
 RA Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimomishi M.,
 RA Sugimura A., Tashiro K., Shimizu S.;
 RT "Molecular cloning and expression of human hepatocyte growth factor.";
 RL Nature 342:440-443 (1989).
 [5]
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=9134393; PubMed=1831266;
 RA Weidner K.M., Arakaki N., Hartmann G., Vandekerckhove J., Weingart S.,
 RA Birmeler W.;
 RT "Evidence for the identity of human scatter factor and human
 hepatocyte growth factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005 (1991).
 [6]
 RN RP SEQUENCE FROM N.A.
 RA Courtney L., Elliot G., Angel S.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 [7]
 RN RP MEDLINE=91369928; PubMed=1832556;
 RX Miyazawa K., Kitamura A., Kitamura N.;
 RT "Structural organization and the transcription initiation site of the
 human hepatocyte growth factor gene.";
 RL Biochemistry 30:9170-9176 (1991).

[8]
 RN RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=9107365; PubMed=1826837;
 RA Yoshiyama Y., Arakaki N., Naka D., Takahashi K., Hirono S., Kondo J.,
 RA Nakayama H., Gohda E., Kitamura N., Teubouch H., Ishii T.,
 RA Hishida T., Daikuhara Y.;
 RT "Identification of the N-terminal residue of the heavy chain of both
 RT native and recombinant human hepatocyte growth factor.";
 RL Biochem. Biophys. Res. Commun. 175:660-667 (1991).
 [9]
 RN RP CARBOHYDRATE-LINKAGE SITE THR-476.
 RX MEDLINE=91329192; PubMed=1482348;
 RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
 RA Nakamura T., Shimizu S.;
 RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
 RT on the alpha chain.";
 RL Biochem. Biophys. Res. Commun. 189:1329-1335 (1992).
 [10]
 RN RP MUTAGENESIS.
 RX MEDLINE=92331602; PubMed=1321034;
 RA Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
 RA Baker J.B., Godowski P.J.;
 RT "Structure-function analysis of hepatocyte growth factor:
 RT identification of variants that lack mitogenic activity yet retain
 RT high affinity receptor binding.";
 RL EMBO J. 11:2503-2510 (1992).
 [11]
 RN RP STRUCTURE BY NMR OF 31-127.
 RX MEDLINE=9815433; PubMed=9493272;
 RA Zhou H., Mazzulla M.J., Kautman J.D., Stahl S.J., Wingfield P.T.,
 RA Rubin J.S., Bottaro D.P., Byrd R.A.;
 RT "The solution structure of the N-terminal domain of hepatocyte growth
 RT factor reveals a potential heparin-binding site.";
 RL Structure 6:109-116 (1998).
 [12]
 RN RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.
 RX MEDLINE=99036858; PubMed=9817840;
 RA Ultsch M., Lokker N.A., Godowski P.J., de Vos A.M.;
 RT "Crystal structure of the NK1 fragment of human hepatocyte growth
 RT factor at 2.0-A resolution.";
 RL Structure 6:1133-1139 (1998).
 CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 CC HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPIC FACTOR, AND ACTS
 CC AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUE AND CELL TYPES.
 CC IT HAS NO DETECTABLE PROTEASE ACTIVITY.
 CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
 CC DISULFIDE BOND.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: Contains 4 kringle domains.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D90334; BAA14348.1; -;
 CC EMBL; D90318; BAA14348.1; JOINED.
 CC EMBL; D90319; BAA14348.1; JOINED.
 CC EMBL; D90320; BAA14348.1; JOINED.
 CC EMBL; D90321; BAA14348.1; JOINED.
 CC EMBL; D90322; BAA14348.1; JOINED.
 CC EMBL; D90323; BAA14348.1; JOINED.
 CC EMBL; D90324; BAA14348.1; JOINED.
 CC EMBL; D90325; BAA14348.1; JOINED.
 CC EMBL; D90326; BAA14348.1; JOINED.
 CC EMBL; D90327; BAA14348.1; JOINED.
 CC EMBL; D90328; BAA14348.1; JOINED.
 CC EMBL; D90329; BAA14348.1; JOINED.
 CC EMBL; D90330; BAA14348.1; JOINED.
 CC EMBL; D90331; BAA14348.1; JOINED.
 CC EMBL; D90332; BAA14348.1; JOINED.

Search completed: January 12, 2004, 17:23:58
Job time : 8.43609 secs

DR EMBL; D90333; BAA14348.1; JOINED.
DR EMBL; M29145; AAAS2650.1; -
DR EMBL; M60718; AAAS2648.1; -
DR EMBL; X16323; CAA34387.1; -
DR EMBL; M73239; AAA64239.1; -
DR EMBL; M73240; AAA64297.1; -
DR EMBL; AC004960; AAC71655.1; -
DR EMBL; M75983; AAG53460.1; -
DR EMBL; M75972; AAG53460.1; JOINED.
DR EMBL; M75973; AAG53460.1; JOINED.
DR EMBL; M75974; AAG53460.1; JOINED.
DR EMBL; M75975; AAG53460.1; JOINED.
DR EMBL; M75976; AAG53460.1; JOINED.
DR EMBL; M75977; AAG53460.1; JOINED.
DR EMBL; M75978; AAG53460.1; JOINED.
DR EMBL; M75979; AAG53460.1; JOINED.
DR EMBL; M75980; AAG53460.1; JOINED.
DR EMBL; M75981; AAG53460.1; JOINED.
DR EMBL; M75982; AAG53460.1; JOINED.
DR PIR; JH0579; JH0579.
DR PDB; 2HGF; 24-JUN-98.
DR PDB; 1BHT; 18-NOV-98.
DR PDB; 1NK1; 29-DEC-99.
DR MEROPS; S01.976; -
DR GlycoSuiteDB; P14210; -
DR Genew; HGNC:4893; HGF.
DR MIM; 142409; -
DR GO; GO:0008083; F:growth factor activity; NAS.
DR GO; GO:0007067; P:mitosis; NAS.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00021; KRINGLE 1; 4.
DR PROSITE; PS0070; KRINGLE 2; 4.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR Growth factor; Kringle; Glycoprotein; Serine protease homology Repeat;
KW Signal; 3D-structure; Polymorphism; Pyroliidone carboxylic acid.
FT SIGNAL 1 31
FT CHAIN 32 494 HEPATOCYTE GROWTH FACTOR ALPHA CHAIN.
FT CHAIN 495 728 HEPATOCYTE GROWTH FACTOR BETA CHAIN.
FT MOD_RES 32 32 PYROLIDONE CARBOXYLIC ACID.
FT DOMAIN 32 127 PAP.
FT DOMAIN 128 206 KRINGLE 1.
FT DOMAIN 211 288 KRINGLE 2.
FT DOMAIN 305 383 KRINGLE 3.
FT DOMAIN 391 463 KRINGLE 4.
FT DOMAIN 495 728 SERINE PROTEASE-LIKE.
FT DISULFID 70 96
FT DISULFID 74 84
FT DISULFID 128 206

Query Match 46.2%; Score 234.5; DB 1; Length 728;
Best Local Similarity 43.4%; Pred. No. 1.5e-18;
Matches 36; Conservative 19; Mismatches 27; Indels 1; Gaps 1;

QY 2 ODCMFGNGKGYRGKTKATVTYVTCQEAQEPHRSFTPIGTWKWAGLEKNGRNPDGDI 61
DB 126 RNCITIGKRSYKGTSTTSKIGICQPMSSNIPHEHS-FLPSSYRGKDQENTCRNPRGSE 184
QY 62 NGPMCYTMNPKLFDYCDIPLCA 84
DB 185 GGPWCFTSNPEVRYEVCIDIPOCS 207

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QY 61 INGPWCYTMNPKLFDYCDIPLCAS 85
DB 71 INGPWCYTMNPKLFDYCDIPLCAA 95

RESULT 2
ID Q15146 PRELIMINARY; PRT; 810 AA.
AC Q15146;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Plasmalogen precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
RA Mitchell D., Robinson J.H.;
RT "Expression of recombinant human plasmalogen and aglycoplasminogen in
Hela cells";
RL Fibrinolysis 0:0-0(1991).
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
EMBL: M74220; AAA36451.1; -.
DR HSP; P00747; 2PK4.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00051; kringle; 5.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR PRODOM; PD000395; PROTHROMBIN.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS50070; KRINGLE_2; 5.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 810 PLASMINOGEN.
SQ SEQUENCE 810 AA; 90555 MW; B05C7D4BD020B3C CRC64;

Query Match 84.6%; Score 430; DB 4; Length 810;
Best Local Similarity 82.4%; Pred. No. 3.4e-41;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYGKATVTGTPCOEWAQEPHRSHTFPGTNKWALEKXNCRNPDGD 60
DB 478 EEDCMFGNGKGYGKATVTGTPCOEWAQEPHRSHTFPGTNKWALEKXNCRNPDGD 537

QY 61 INGPWCYTMNPKLFDYCDIPLCAS 85
DB 538 VGGPWCYTMNPKLFDYCDIPLCAA 562

RESULT 3
ID Q91WJ5 PRELIMINARY; PRT; 812 AA.
AC Q91WJ5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Plasmalogen.
GN PUG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Bratwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
RA Nagara R.;
RT "Genomic Sequence Analysis in the Mouse t-complex Region";
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
EMBL: BC014773; AAH14773.1; -.
DR EMBL; AF481053; AAM22156.1; -.
DR HSP; P00761; IAN1.
DR MGD; MGI:97620; P1g.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Prothrombin.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR001400; Somatostatin.
DR Pfam: PF00051; kringle; 5.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR PRODOM; PD000395; PROTHROMBIN.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS50070; KRINGLE_2; 5.
DR PROSITE; PS00338; SOMATOSTATIN_2; 1.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 812 AA; 90781 MW; 2417326E6A2FED2 CRC64;

Query Match 81.3%; Score 413; DB 11; Length 812;
Best Local Similarity 80.2%; Pred. No. 3.1e-39;
Matches 69; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYGKATVTGTPCOEWAQEPHRSHTFPGTNKWALEKXNCRNPDGD 60
DB 478 EIDCMFGNGKGYGKATVTGTPCOEWAQEPHRSHTFPGTNKWALEKXNCRNPDGD 537

QY 61 INGPWCYTMNPKLFDYCDIPLCAS 86
DB 538 VGGPWCYTMNPKLFDYCDIPLCAA 563

RESULT 4
ID Q9R0W3 PRELIMINARY; PRT; 812 AA.
AC Q9R0W3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Plasmalogen protein precursor (EC 3.4.21.7).
GN PLASMINOGEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Bangert K., Johnsen A.H., Thorsen S.;
RT "Rat plasminogen: cDNA and gene structure.";
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=91250378; PubMed=1645711;
RA Kanalaas J.U., Makker S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
RT receptor site for plasminogen.";
RL J. Biol. Chem. 266:10825-10829(1991).
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL: AJ242649; CAB46014.1; -.
DR HSSP: P00747; 1PMK.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan app.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00051; Kringle; 5.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR PRODOM: PD000395; Kringle; 5.
DR SMART: SM00130; KR; 4.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00021; KRINGLE_1; 5.
DR PROSITE: PS00070; KRINGLE_2; 5.
DR PROSITE: PS00338; SOMATOSTATIN_2; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR GlycoProtein; Hydrolase; Kringle; Protease; Serine protease; Signal.
FT SIGNAL
FT CHAIN
FT SEQUENCE 812 AA; 90535 MW; 8C703C51410EBC9E CRC64;

Query Match 80.3%; Score 408; DB 11; Length 812;
Best Local Similarity 80.0%; Pred. No. 1.2e-38;
Matches 68; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 BDDCMGNGKGYRGKATVTGTPCOEMAQEPHSHSTFIPGNNKAGLEKKNYCRNPDGD 60
DB 478 EIDCMGNGKGYRGKATVTGTPCOEMAQEPHSHSTFIPGNNKAGLEKKNYCRNPDGD 537

QY 61 INGPWCYTANPRKLFYCDIPLCAS 85
DB 538 VNGPWCYTANPRKLFYCDIPLCAS 562

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RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cox L.A., Jett C., Hixson J.E.;
RT "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
RT Site Mutation is Associated with Deletion of a Single Exon in a Null
RT Allele.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL: AF029692; AAB97887.1; -.
DR HSSP: P00747; 5HPG.
DR MEROPS: S01.233; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00051; Kringle; 1.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00024; PAN; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR PRODOM: PD000395; Kringle; 1.
DR SMART: SM00130; KR; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS00070; KRINGLE_2; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR GlycoProtein; Hydrolase; Kringle; Protease; Serine protease.
FT NON TER
FT SEQUENCE 334 AA; 36791 MW; C7DC06E03B965286 CRC64;

Query Match 79.5%; Score 404; DB 6; Length 334;
Best Local Similarity 81.0%; Pred. No. 1.3e-38;
Matches 68; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 3 DCMFGNGKGYRGKATVTGTPCOEMAQEPHSHSTFIPGNNKAGLEKKNYCRNPDGD 62
DB 4 DCMFGNGKGYRGKATVTGTPCOEMAQEPHSHSTFIPGNNKAGLEKKNYCRNPDGD 63

QY 63 GPWCYTANPRKLFYCDIPLCAS 86
DB 64 GPWCYTANPRKLFYCDIPLCAS 87

RESULT 6
018783
ID 018783; PRELIMINARY; PRT; 806 AA.
AC 018783;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Plasminogen.
OS Macropus eugenii (Tammam wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_Taxid=9315;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=98004511; PubMed=9342350;
RA Lawn R.M., Schwartz K., Patchy L.;
RT "Convergent evolution of Apolipoprotein(a) in primates and hedgehog.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL: AF012297; AAB65760.1; -.
DR HSSP: P00747; 5HPG.
DR MEROPS: S01.233; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan app.
DR InterPro: IPR003966; Prothrombin.

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DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00051; kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle; 5.
 DR SMART: SM00130; KR; 4.
 DR SMART: SM00473; PAN_Ap; 1.
 DR SMART: SM00020; TRYP_Spc; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS00070; KRINGLE_2; 5.
 DR PROSITE: PS00240; TRYPsin Dom; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR GlycoProtein: Hydrolase; Kringle; Protease; Serine protease.
 KW GlycoProtein: Hydrolase; Kringle; Protease; Serine protease.
 SQ SEQUENCE 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;

Query Match 74.6%; Score 379; DB 6; Length 806;
 Best Local Similarity 74.1%; Pred. No. 2.7e-35;
 Matches 63; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATVTGTGTCQEWAAQEPHRSFTFGTNKMALEKNCYCRNPDDG 60
 DB 473 ESDCMGSGKDYRGKSTVTGTLCAWTAQEPHRSFTFGTDYPPAGLEENYCRNPDDG 532
 QY 61 INGPWCYTNMPRLFDYCDIPLCAS 85
 DB 533 PNGPWCYTNMPKLFYCDIPLCAS 557

RESULT 7

Q8AVB0 PRELIMINARY; PRT; 429 AA.
 AC Q8AVB0;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Plasmidogen precursor (Fragment).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hanumanthiah R., Day K., Jagadeeswaran P.;
 RT "Comprehensive analysis of blood coagulation pathways in teleostei";
 RT Evolution of coagulation factor genes and identification of zebrafish
 RT factor VIII.";
 RL Blood Cells Mol. Dis. 0:0-0(2002).
 DR EMBL; AF515276; AA071006.1; -.
 FT NON_TER 1
 SQ SEQUENCE 429 AA; 47556 MW; 9A580A214A549C12 CRC64;

Query Match 56.1%; Score 285; DB 13; Length 429;
 Best Local Similarity 55.3%; Pred. No. 1e-24;
 Matches 47; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATVTGTGTCQEWAAQEPHRSFTFGTNKMALEKNCYCRNPDDG 60
 DB 99 EKDCKNGNGAEYRGSTSMNTMGVTCQAWRMTFHQHASFTFTHPDKGLSNGCRNPDDSD 158
 QY 61 INGPWCYTNMPRLFDYCDIPLCAS 85
 DB 159 VNGPWCYTTDPSSKMDYCOIPDCBS 183

RESULT 8
 Q8WMR1 PRELIMINARY; PRT; 359 AA.
 ID Q8WMR1;
 AC Q8WMR1;

DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Plasmidogen (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pirte-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O.,
 RA Folkman J., Waters D.J.;
 RT "Angiotensin is detectable in the urine of dogs with spontaneous Bone
 RT Cancer.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 DR EMBL; AY069985; AA158519.1; -.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003966; Prothrombin.
 DR Pfam: PF00051; Kringle; 4.
 DR PRINTS: PR00018; KRINGLE.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle; 4.
 DR SMART: SM00130; KR; 4.
 DR PROSITE: PS00021; KRINGLE_1; 4.
 DR PROSITE: PS00070; KRINGLE_2; 4.
 KW Glycoprotein; Kringle.
 FT NON_TER 1
 FT NON_TER 359
 SQ SEQUENCE 359 AA; 41172 MW; 776D35F4AB0BDD9E CRC64;

Query Match 49.3%; Score 250.5; DB 6; Length 359;
 Best Local Similarity 53.1%; Pred. No. 8.4e-21;
 Matches 43; Conservative 8; Mismatches 29; Indels 1; Gaps 1;

QY 3 DCMFGNGKGYRGKATVTGTGTCQEWAAQEPHRSFTFGTNKMALEKNCYCRNPDDG 62
 DB 5 ECKTGNGKTYRGTMATKNDVACQKWDNSPHK-PYTPBKPLLEENYCRNPDDEN 63
 QY 63 GPCWCTNMPRLFDYCDIPLC 83
 DB 64 GPCWCTNMPRLFDYCDIPLC 84

RESULT 9

Q9PU78 PRELIMINARY; PRT; 313 AA.
 AC Q9PU78;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hepatocyte growth factor-like protein (Fragment).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylia; Crocodylinae; Crocodylus.
 NCBI_TaxID=8501;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Liver;
 RX MEDLINE=20022983; PubMed=10555283;
 RA Hughes S., Zelus D., Mouchiroud D.;
 RT "Warm-blooded isochore structure in nile crocodile and turtle.";
 RL Mol. Biol. Evol. 16:1521-1527(1999).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL; AJ011396; CAB56422.1; -.
 DR HSSP; P00747; IHPU.
 DR MEROPS; S01.977; -.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00051; Kringle; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00018; KRINGLE.

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Qy      2  QDGMFGNGKGYRGKATVTTGTGTPCOEWAQEPHRHSTFIPGTNKNAGLEKNCYCNPDGDI 61
Db      377  EGCYHSGSGEGRVGSVSTRKRGVOCQHWSSETPHK-PQFTPTSAAPHAGLEANFCNPDGDS 435
Matches 40; Conservative 19; Mismatches 27; Indels 1; Gaps 1;

Qy      62  NGPCYTMNPRKLFDCYDIPLC 83
Db      436  HGPWCYTLDEPTLFDYCALRGC 457

RESULT 11
ID      Q90ZN6      PRELIMINARY;      PRT;      709 AA.
AC      Q90ZN6;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Hepatocyte growth factor-like 1.
GN      MST1 OR HGFL.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
CC      Cyprinidae; Danio.
OX      NCBI_TaxId=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Baasett D.I., Wilson S.W.;
RT      "Early expression of zebrafish Hepatocyte Growth Factor-Like 1
RL      suggests a conserved role in vertebrate neural induction.";
RL      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 51.
CC      -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR      EMBL; AF370035; AAK54207.1; -.
DR      HSSP; P00761; IAN1.
DR      ZFIN; ZDB-GENE-020806-3; met1.
DR      InterPro; IPR001314; Chymotrypsin.
DR      InterPro; IPR000001; Kringle.
DR      InterPro; IPR003014; PAN.
DR      InterPro; IPR003609; Pan_app.
DR      InterPro; IPR01254; Ser_protease_Try.
DR      Pfam; PF00051; kringle; 4.
DR      Pfam; PF00024; PAN_1.
DR      Pfam; PF00089; trypsin; 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      PRINTS; PR00018; KRINGLE.
DR      ProDom; PD000395; Kringle; 4.
DR      SMART; SM00130; KR; 4.
DR      SMART; SM00473; PAN_AP; 1.
DR      SMART; SM00020; TRY_PSC; 1.
DR      PROSITE; PS00021; KRINGLE_1; 4.
DR      PROSITE; PS50070; KRINGLE_2; 4.
DR      PROSITE; PS50240; TRYPSIN_DOM; 1.
KM      GLYCOPROTEIN; Hydrolase; Kringle; Protease; Serine protease.
SQ      SEQUENCE 709 AA; 81271 MW; 9907236C5DB73A20 CRC64;

Query Match      47.3%; Score 240.5; DB 13; Length 709;
Best Local Similarity 51.2%; Pred. No. 2,6e-19;
Matches 41; Conservative 12; Mismatches 24; Indels 3; Gaps 1;

Qy      4  CMFGNGKGYRGKATVTTGTGTPCOEWAQEPHRHSTFIPGTNKNAGLEKNCYCNPDGDI 63
Db      111  CTVGKGDYGVKSVTTSIGRTCCQWMSKFPYHDMWTSATN---GLELNTCRNPDGDRIG 167
Matches 41; Conservative 12; Mismatches 24; Indels 3; Gaps 1;

Qy      64  PWCYTMNPRKLFDCYDIPLC 83
Db      168  PWCYTMNPRKLFDCYDIPLC 187
Matches 41; Conservative 12; Mismatches 24; Indels 3; Gaps 1;

RESULT 12

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091XG8
ID 091XG8 PRELIMINARY; PRT; 716 AA.
AC 091XG8;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Hepatocyte growth factor-like.
GN HGFL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Straubeberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR EMBL; BC010551; AAH10551.1; -.
DR HSSP; P00761; 1AN1.
DR MGD; MGI:96080; HGFL.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR003966; Prothrombin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; TRY_PPC; 1.
DR SMART; SM00020; TRY_PPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS50070; KRINGLE_2; 4.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR GlycoProtein; Hydrolase; Kringle; Protease; Serine protease.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 716 AA; 80693 MW; 12474C48A7D4B46D CRC64;

Query Match 47.1%; Score 239.5; DB 11; Length 716;
Best Local Similarity 48.8%; Pred. No. 3.4e-19;
Matches 40; Conservative 14; Mismatches 27; Indels 1; Gaps 1;

QY 2 QDCMFGNGKGRGKATTTGTPCQEWAAQEPHSHSTFPGTNKAGLEKNYCRNPDGDI 61
DB 377 EGCYHSGEGYRGSVSKTRKGVCCQHWSSSTPHK-PQFTLSAPQAGLEANPCRNPDGDS 435
QY 62 NGPMCTYMNPRKLPDYCDIPLC 83
DB 436 HGPWCYTLDPDILFDYCALQRC 457

RESULT 13
Q28398 PRELIMINARY; PRT; 2869 AA.
AC Q28398;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Apolipoprotein(a) (Fragment).
OS Erinnaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
OX NCBI_TaxID=3365;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=96025778; PubMed=7592597;
RA Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,

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RA Byrne C.D., Fong K.J., Meer K., Patchy L.;
RT "The recurring evolution of lipoprotein(a). Insights from cloning of
RT hedgehog apolipoprotein(a)."
RL J. Biol. Chem. 270:24004-24009(1995).
CC -1- SIMILARITY: CONTAINS 31 KRINGLE DOMAINS.
DR EMBL; U33170; AAC48522.1; -.
DR HSSP; P00747; 1PMK.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 31.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 31.
DR SMART; SM00130; KR; 31.
DR PROSITE; PS00021; KRINGLE_1; 30.
DR PROSITE; PS50070; KRINGLE_2; 31.
KW Glycoprotein; Kringle; Lipoprotein.
FT NON TER 1
SQ SEQUENCE 2869 AA; 318601 MW; 9527CEP85A4FB2A CRC64;

Query Match 47.0%; Score 239; DB 6; Length 2869;
Best Local Similarity 50.6%; Pred. No. 1.8e-18;
Matches 43; Conservative 9; Mismatches 31; Indels 2; Gaps 2;

QY 2 QDCMFGNGKGRGKATTTGTPCQEWAAQEPHSHSTFPGTNKAGLEKNYCRNPDGDI 61
DB 2589 EGCLENGENYQGNMAYTSGPCQGRKQTPRHQ-YTPENYPSKNLGNYCRNPDGDI 2647
QY 62 NGPMCTYMNPRKLPDYCDIPLCASS 86
DB 2648 -APWCYTNMAYRWECSIPTCESS 2671

RESULT 14
Q13208 PRELIMINARY; PRT; 567 AA.
AC Q13208;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Hepatocyte growth factor-like protein homolog.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20191171; PubMed=10728827;
RA Degen S.J.F., McDowell S.A., Waltz S.B., Gould F., Stuart L.A.,
RA Carritt B.;
RT "Structure of the human DIP151A locus: a chromosome 1 locus with 978
RT identity to the chromosome 3 gene coding for hepatocyte growth factor-
RT like protein."
RL DNA Seq. 8:409-413(1998).
CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR EMBL; U28054; AAC63092.1; -.
DR HSSP; P00747; 2PK4.
DR MEROPS; S01.977; -.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00020; TRY_PPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 3.
DR PROSITE; PS50070; KRINGLE_2; 4.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 567 AA; 64117 MW; 3FC38B07F1645810 CRC64;

Query Match 46.8%; Score 237.5; DB 4; Length 567;
Best Local Similarity 50.6%; Pred. No. 4.5e-19;

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Matches 42; Conservative 12; Mismatches 28; Indels 1; Gaps 1;

QY 2 QDCMFGNGKGYRGKATTTGTGTCQEMAAOEPRHSTFIPTNKWAGLEKNYCRNPDGDI 61
 DB 343 QDCIHAGAGEYRTGTVSKTRKGVOCQKMSATPHK-PQFTFTSEPHAQLEENFCQNPDS 401
 QY 62 NGPWCYTMNPKLFDYCDIPLCA 84
 DB 402 HGPWCYTMDBRTPFDYCALRCA 424

RESULT 15

Q91402 PRELIMINARY; PRT; 710 AA.
 ID Q91402;
 AC Q91402;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hepatocyte growth factor.
 GN HGF.
 OS Xenopus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae.
 OX NCBI_TaxID=8353;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tail bud;
 RX MEDLINE=95267690; PubMed=7748783;
 RA Nakamura H., Tashiro K., Nakamura T., Shiohawa K.;
 RT "Molecular cloning of Xenopus HGF cDNA and its expression studies in
 RT Xenopus early embryogenesis.";
 RL Mech. Dev. 49:123-131(1995)
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 DR EMBL: S77422; AAB34354.2; -.
 DR HSSP: P14210; 1BHT.
 DR MEROPS: S01.976; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00051; kringle; 4.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PRO0018; KRINGLE.
 DR ProDom: PD000395; Kringle; 4.
 DR SMART: SM00130; KR; 4.
 DR SMART: SM00473; PAN_AB; 1.
 DR SMART: SM00020; TRY_SPC; 1.
 DR PROSITE: PS00021; KRINGLE_1; 4.
 DR PROSITE: PS50070; KRINGLE_2; 4.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR Glycoprotein: Hydrolase; Kringle; Protease; Serine protease.
 KW SEQUENCE 710 AA; 81487 MW; 5F6480BE31C27FC CRC64;

Query Match 46.8%; Score 237.5; DB 13; Length 710;
 Best local Similarity 47.0%; Pred. No. 5.8e-19;
 Matches 39; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

QY 2 QDCMFGNGKGYRGKATTTGTGTCQEMAAOEPRHSTFIPTNKWAGLEKNYCRNPDGDI 61
 DB 113 RDCIHAGAGEYRTGTVSKTRKGVOCQKMSATPHK-PQFTFTSEPHAQLEENFCQNPDS 171
 QY 62 NGPWCYTMNPKLFDYCDIPLCA 84
 DB 172 GGPWCYTKSPVRHVDVCDIPCS 194

Search completed: January 12, 2004, 17:25:37
 Job time : 27.4812 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 17:16:07 ; Search time 34.2707 Seconds
(without alignments)
398.314 Million cell updates/sec

Title: US-10-088-548-8

Perfect score: 508
Sequence: 1 BDDCMFGNGKGRKATTV.....YTMNPKLPDYCDIPLCASS 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: A_Genseq_19Jun03:*
2: /SIDSI/gcgdata/genseq/genseq-emb1/AA1980.DAT:*
3: /SIDSI/gcgdata/genseq/genseq-emb1/AA1981.DAT:*
4: /SIDSI/gcgdata/genseq/genseq-emb1/AA1982.DAT:*
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6: /SIDSI/gcgdata/genseq/genseq-emb1/AA1984.DAT:*
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13: /SIDSI/gcgdata/genseq/genseq-emb1/AA1991.DAT:*
14: /SIDSI/gcgdata/genseq/genseq-emb1/AA1992.DAT:*
15: /SIDSI/gcgdata/genseq/genseq-emb1/AA1993.DAT:*
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21: /SIDSI/gcgdata/genseq/genseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/genseq/genseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/genseq/genseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/genseq/genseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------------------|
| 1 | 508 | 100.0 | 86 | 22 | AA172947 Human apolipoprotein |
| 2 | 508 | 100.0 | 91 | 20 | AA142303 Human apolipoprotein |
| 3 | 508 | 100.0 | 308 | 12 | AA172944 Human angiotensin |
| 4 | 432 | 85.0 | 380 | 13 | AA172504 [GARSQ] - [Plasmino |
| 5 | 432 | 85.0 | 476 | 13 | AA172503 [GARSQ] - [Plasmino |
| 6 | 432 | 85.0 | 810 | 22 | AA167228 Amino acid sequenc |
| 7 | 430 | 84.6 | 90 | 21 | AA1601914 Human plasminogen |
| 8 | 430 | 84.6 | 91 | 21 | AA158868 Human plasminogen |
| 9 | 430 | 84.6 | 93 | 21 | AA1601317 Human plasminogen |

| | | | | | |
|----|-----|------|-----|----|-----------------------------|
| 10 | 430 | 84.6 | 95 | 21 | AA1601913 Human plasminogen |
| 11 | 430 | 84.6 | 98 | 21 | AA1601916 Human plasminogen |
| 12 | 430 | 84.6 | 101 | 18 | AA134286 Human kring 5 pe |
| 13 | 430 | 84.6 | 101 | 21 | AA1601890 Human plasminogen |
| 14 | 430 | 84.6 | 101 | 21 | AA1601912 Human plasminogen |
| 15 | 430 | 84.6 | 104 | 21 | AA1601915 Human plasminogen |
| 16 | 430 | 84.6 | 189 | 21 | AA1601918 Human plasminogen |
| 17 | 430 | 84.6 | 192 | 21 | AA1601919 Human plasminogen |
| 18 | 430 | 84.6 | 266 | 22 | AA1601919 Human plasminogen |
| 19 | 430 | 84.6 | 266 | 22 | AA1601919 Human plasminogen |
| 20 | 430 | 84.6 | 266 | 22 | AA1601919 Human plasminogen |
| 21 | 430 | 84.6 | 271 | 21 | AA1601919 Human plasminogen |
| 22 | 430 | 84.6 | 348 | 23 | AA1601919 Human plasminogen |
| 23 | 430 | 84.6 | 357 | 23 | AA1601919 Human plasminogen |
| 24 | 430 | 84.6 | 362 | 23 | AA1601919 Human plasminogen |
| 25 | 430 | 84.6 | 437 | 19 | AA1601919 Human plasminogen |
| 26 | 430 | 84.6 | 484 | 24 | AA1601919 Human plasminogen |
| 27 | 430 | 84.6 | 566 | 20 | AA1601919 Human plasminogen |
| 28 | 430 | 84.6 | 790 | 15 | AA1601919 Human plasminogen |
| 29 | 430 | 84.6 | 790 | 22 | AA1601919 Human plasminogen |
| 30 | 430 | 84.6 | 791 | 21 | AA1601919 Human plasminogen |
| 31 | 430 | 84.6 | 791 | 21 | AA1601919 Human plasminogen |
| 32 | 430 | 84.6 | 791 | 21 | AA1601919 Human plasminogen |
| 33 | 430 | 84.6 | 791 | 22 | AA1601919 Human plasminogen |
| 34 | 430 | 84.6 | 791 | 23 | AA1601919 Human plasminogen |
| 35 | 430 | 84.6 | 791 | 23 | AA1601919 Human plasminogen |
| 36 | 430 | 84.6 | 810 | 11 | AA1601919 Human plasminogen |
| 37 | 430 | 84.6 | 810 | 12 | AA1601919 Human plasminogen |
| 38 | 430 | 84.6 | 810 | 14 | AA1601919 Human plasminogen |
| 39 | 430 | 84.6 | 810 | 20 | AA1601919 Human plasminogen |
| 40 | 430 | 84.6 | 810 | 20 | AA1601919 Human plasminogen |
| 41 | 430 | 84.6 | 810 | 21 | AA1601919 Human plasminogen |
| 42 | 430 | 84.6 | 810 | 21 | AA1601919 Human plasminogen |
| 43 | 430 | 84.6 | 810 | 23 | AA1601919 Human plasminogen |
| 44 | 430 | 84.6 | 810 | 23 | AA1601919 Human plasminogen |
| 45 | 430 | 84.6 | 810 | 23 | AA1601919 Human plasminogen |

ALIGNMENTS

RESULT 1
ID AA172947 standard; Protein; 86 AA.
AA172947;
XX
AC AA172947;
XX
XX
DT 13-JUN-2001 (first entry)
XX
DE Human apolipoprotein(a) kring 5 domain V38, LK8 protein.
XX
XX Human, angiotensin inhibitor; LK8; apolipoprotein(a) kring 5 domain;
KW angiotensin-mediated disease; cancer; rheumatoid arthritis; therapy;
KW cystic; antithrombotic; antitumor; antiproliferative; psoriasis;
KW ocular angiogenic disease; endothelial cell proliferation; tumor;
KW cell migration.
XX
XX Homo sapiens.
OS
XX
XX WO200119868-A1.
PN
XX
XX 22-MAR-2001.
PD
XX
XX 15-SEP-1999; 99WO-KR00554.
PF
XX
XX 15-SEP-1999; 99WO-KR00554.
PR
XX
XX 15-SEP-1999; 99WO-KR00554.
PA
XX
XX (MOGA-) MOGA BIOTECHNOLOGY RES INST.
PI Chang J, Kim JS, Park EJ, Yum J, Chung S;
DR WPI; 2001-244787/25.
N-PSDB; AAD03258.

XX Novel angiogenesis inhibitor. LK68 for treating angiogenesis-mediated
PT diseases, e.g. cancer and rheumatoid arthritis, has human
PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
PT sequence -

PS Claim 3; Page 47; 50pp; English.

XX The present sequence is human LK6 protein which contains the amino
CC acid sequence of human apolipoprotein(a) kringle domain V38
CC (KV38). The human apolipoprotein(a) kringle domains IV36 (LK6
CC protein), IV37 (LK7 protein) and V38 (LK8 protein) together form the
CC angiogenesis inhibitor. LK68 protein. LK68, LK6, LK7 and LK8 are
CC inhibitors of endothelial cell proliferation, cell migration and
CC normal development of capillaries in the chick embryo chorioallantoic
CC membrane (CAM). LK68 protein, its single kringle or their functional
CC equivalents, are useful for treating angiogenesis-mediated diseases,
CC such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic
CC disease in animals or humans. LK68 is useful as an anticancer agent and
CC also for inhibiting primary tumour growth.

SQ Sequence 86 AA;

Query Match 100.0%; Score 508; DB 22; Length 86;
Best Local Similarity 100.0%; Pred. No. 1e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EODCMFGNGKGYRGKATTTGTPCOEWAQBPBRHSTFTPTNKVAGLEKATCRPPDD 60
DB 1 EODCMFGNGKGYRGKATTTGTPCOEWAQBPBRHSTFTPTNKVAGLEKATCRPPDD 60
61 INGPWCYTNNPKRLFDYCDIPLCASS 86
DB 61 INGPWCYTNNPKRLFDYCDIPLCASS 86

RESULT 2

AAV42303
ID AAV42303 standard; protein; 91 AA.

AC AAV42303;

DT 06-DEC-1999 (first entry)

XX Human apolipoprotein A kringle 5 domain.

KW Apolipoprotein A; apo(a); glycoprotein; heart disease; antibody;
KM detection; diagnosis.

XX Homo sapiens.

OS Homo sapiens.

PN W09936784-A1.

PD 22-JUL-1999.

XX 20-JAN-1999; 99WO-US01211.

XX 20-JAN-1998; 98US-0072924.

XX (ABBO) ABBOTT LAB.

PI Kundu SK, Ziemann R;

XX WPI; 1999-571560/48.

XX New methods for measuring concentrations of lipoprotein(a) in a plasma
PT sample -

XX Disclosure; Page 68; 71pp; English.

XX This sequence represents the kringle 5 domain of human apolipoprotein A
CC (apo(a)), which was used to generate monoclonal antibodies. Apo(a) is a
CC characteristic glycoprotein component of lipoprotein(a) (Lp(a)), which

CC is not found in the otherwise identical low density lipoprotein (LDL).
CC Lp(a) and LDL are both associated with premature coronary heart disease.
CC Increased Lp(a) concentrations may inhibit fibrinolysis by reducing the
CC generation of plasmin. This may be effected by competition for
CC plasminogen cell-surface receptors, by inhibition of activation of
CC plasminogen, or by competition for binding sites on fibrin. Anti-apo(a)
CC antibodies can be used in a novel method of Lp(a) quantitation. Such
CC antibodies are not cross-reactive with plasminogen, LDL, and the various
CC types of apo(a) kringle 4 domains. Previous methods of Lp(a) immunoassay
CC used antibodies that bind to the apo(a) kringle 4 domain, which is
CC present in multiple copies. One method, TERMO ELISA (enzyme-linked
CC immunosorbent assay), tended to produce erroneous results with cardiac
CC and diabetic patients, especially those with very high Lp(a)
CC concentrations (greater than 50 mg/dl). Apo(a) monoclonal antibodies may
CC serve as accurate markers for the detection and diagnosis of heart
CC disease.

SQ Sequence 91 AA;

Query Match 100.0%; Score 508; DB 20; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EODCMFGNGKGYRGKATTTGTPCOEWAQBPBRHSTFTPTNKVAGLEKATCRPPDD 60
DB 3 EODCMFGNGKGYRGKATTTGTPCOEWAQBPBRHSTFTPTNKVAGLEKATCRPPDD 62
61 INGPWCYTNNPKRLFDYCDIPLCASS 86
DB 63 INGPWCYTNNPKRLFDYCDIPLCASS 88

RESULT 3

AAV72944
ID AAV72944 standard; Protein; 308 AA.

AC AAV72944;

DT 13-JUN-2001 (first entry)

XX Human angiogenesis inhibitor, LK68 protein.

XX Human; angiogenesis inhibitor; LK68; apolipoprotein(a) kringle domain;

KW angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy;

KW cytostatic; antineumatic; antiarthritic; antipsoriatic; psoriasis;

KW ocular angiogenic disease; endothelial cell proliferation; tumour;

XX cell migration.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

| | | |
|-----------|---|---|
| XX | Chang J, Kim JS, Park EJ, Yum J, Chung S; | |
| PI | | |
| XX | WPI, 2001-244787/25. | |
| DR | N-PSDB; AAD03255. | |
| XX | | |
| XX | Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated | |
| PT | diseases, e.g. cancer and rheumatoid arthritis, has human | |
| PT | apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid | |
| PT | sequence | |
| XX | | |
| PS | Claim 4; Page 42-44; 50pp; English. | |
| XX | | |
| CC | The present sequence is human angiogenesis inhibitor, LK68 protein. | |
| CC | LK68 protein contains the amino acid sequences of human apolipoprotein(a) | |
| CC | kringle domains IV36 (LK6 protein), IV37 (LK7 protein) and V38 | |
| CC | (LK8 protein). LK68, LK6, LK7 and LK8 are inhibitors are of endothelial | |
| CC | cell proliferation, cell migration and normal development of capillaries | |
| CC | in the chick embryo chorioallantoic membrane (CAM). LK68 protein, its | |
| CC | single kringles or their functional equivalents, are useful for | |
| CC | treating angiogenesis-mediated diseases, such as cancer, rheumatoid | |
| CC | arthritis, psoriasis or ocular angiogenic disease in animals or humans. | |
| CC | LK68 is useful as an anticancer agent and also for inhibiting primary | |
| CC | tumour growth. | |
| XX | | |
| SO | Sequence 308 AA; | |
| | | |
| | Query Match 100.0%; Score 508; DB 22; Length 308; | |
| | Best Local Similarity 100.0%; Pred. No. 3.5e-42; | |
| | Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Oy | 1 EODCMFGNGKGYRGKATTTTGTGTCOEWAAGPHHSHFTPTGNTKAGLEKNYCNPDGD 60 | |
| Db | 223 EODCMFGNGKGYRGKATTTTGTGTCOEWAAGPHHSHFTPTGNTKAGLEKNYCNPDGD 282 | |
| Oy | 61 INGPWCYTMNPRKLEFDYCDIPLCASS 86 | |
| Db | 283 INGPWCYTMNPRKLEFDYCDIPLCASS 308 | |
| | | |
| RESULT 4 | | |
| AAAR22504 | | |
| ID | AAAR22504 standard; Protein; 380 AA. | |
| XX | | |
| AC | AAAR22504; | |
| XX | | |
| DT | 09-JAN-2003 (updated) | |
| DT | 25-AUG-1992 (first entry) | |
| XX | | |
| DE | [GARSYQ] - [Plasminogen 443-541] - [u-PA 137-411] hybrid. | |
| XX | | |
| KW | Plasminogen; urokinase-like plasminogen activator; hybrid; | |
| KW | fibrinolysis; blood clotting; acute myocardial infarction. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| Key | | |
| FT | Region | Location/Qualifiers |
| FT | | 1..6 |
| FT | Region | /note= "amino acids -3 to +3 of C-PA" |
| FT | Region | 7..105 |
| FT | Region | /note= "amino acids 443-541 of plasminogen" |
| FT | Region | 106..380 |
| FT | | /note= "amino acids 137-411 of u-PA" |
| FT | Cleavage-site | 126..127 |
| FT | | /note= "u-PA cleavage site" |
| XX | | |
| FN | W09204450-A. | |
| XX | | |
| PD | 19-MAR-1992. | |
| XX | | |
| PF | 29-AUG-1991; | 91WO-GB01455. |
| XX | | |
| PR | 01-SEP-1990; | 90GB-0019120. |

| | |
|--------------------------|---|
| XX | (BEEC) BEECHAM GROUP PLC. |
| PA | |
| XX | |
| PI | Dodd I, Brown M, Robinson JH; |
| XX | |
| DR | WPI, 1992-114357/14. |
| XX | |
| PT | Hybrid plasminogen activators for treating thrombotic diseases - |
| PT | comprise Kringles 5 or Kringles 4 and 5 of plasminogen linked to |
| PT | B-chain of t-PA or u-PA via aminoacid sequence |
| XX | |
| PS | Claim 11; Page 50; 64pp; English. |
| XX | |
| CC | This hybrid plasminogen/u-PA sequence is described in the |
| CC | specification although the sequence itself is not given. The |
| CC | sequence given here has been compiled using the human plasminogen |
| CC | sequence from Patent No. WO9013640 and the human u-PA sequence |
| CC | from the SWISSPROT database (UROKSHUMAN). The hybrid fibrinolytic |
| CC | enzyme are useful in the treatment of thrombotic diseases. |
| CC | See also R24299, R22502 and R22503. |
| CC | (Updated on 09-JAN-2003 to add missing OS field.) |
| XX | |
| SO | Sequence 380 AA; |
| Query March | 85.0%; Score 432; DB 13; Length 380; |
| Best Local Similarity | 82.6%; Pred. No. 1.3e-34; |
| Matches 71; Conservative | 6; Mismatches 9; Indels 0; Gaps 0; |
| OY | 1 EQDCMFGNGKGYRKKATVTVGTCQEWAAQDEPHRHSTFIPGTNKWAGLEKNYCRNPDDG 60 |
| DB | 23 EEDCMFGNGKGYRKKRATTVTGTCQDWAQDEPHRHSTFIPETNPRGLEKNYCRNPDDG 82 |
| OY | 61 IWPWCYTTMNPRLFDYCDIPLCASS 86 |
| DB | 83 VGGWCYTTMNPRLDYCDVQCPSS 108 |
| RESULT 5 | |
| AAR22503 | |
| ID | AAR22503 standard; Protein; 476 AA. |
| XX | |
| AC | AAR22503; |
| XX | |
| DT | 09-JAN-2003 (updated) |
| DT | 25-AUG-1992 (first entry) |
| XX | |
| DE | [GARSYQ] - [Plasminogen 347-541] - [u-PA 137-411] hybrid. |
| XX | |
| KM | Plasminogen; urokinase-like plasminogen activator; hybrid; |
| KW | fibrinolysis; blood clotting; acute myocardial infarction. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| EH | Key |
| FT | Region |
| FT | Location/Qualifiers |
| FT | 1..6 |
| FT | /note= "amino acids -3 to +3 of t-PA" |
| FT | 7..201 |
| FT | /note= "amino acids 347-541 of plasminogen" |
| FT | 202..476 |
| FT | /note= "amino acids 137-411 of u-PA" |
| FT | 222..223 |
| FT | /note= "u-PA cleavage site" |
| XX | |
| XX | WO9204450-A. |
| XX | |
| PD | 19-MAR-1992. |
| XX | |
| PF | 29-AUG-1991; 91WO-GB01455. |
| XX | |
| PR | 01-SEP-1990; 90GB-0019120. |
| XX | |
| PA | (BEEC) BEECHAM GROUP PLC. |
| XX | |

PI Dodd I, Brown M, Robinson JH;
XX WPI, 1992-114357/14.
XX
XX Hybrid plasminogen activators for treating thrombotic diseases -
PT comprise Kringles 5 or Kringles 4 and 5 of plasminogen linked to
PT B-chain of t-PA or u-PA via aminoacid sequence
XX
PS Claim 10; Page 50; 64pp; English.
XX
XX This hybrid plasminogen/u-PA sequence is described in the
CC specification although the sequence itself is not given. The
CC sequence given here has been compiled using the human plasminogen
CC sequence from Patent No. WO9013640 and the human u-PA sequence
CC from the SWISSPROT database (UROS\$HUMAN). The hybrid fibrinolytic
CC enzymes are useful in the treatment of thrombotic diseases.
CC See also R22499, R22502 and R22504.
CC (Updated on 09-JAN-2003 to add missing OS field.)
XX
SQ Sequence 476 AA;
Query Match 85.0%; Score 432; DB 13; Length 476;
Best Local Similarity 82.6%; Pred. No. 1.7e-34;
Matches 71; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
QY 1 EDDCMFNGNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNKAGLEKXNCRNPDG 60
DB 119 EDDCMFNGNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNKAGLEKXNCRNPDG 178
QY 61 INGPWCYTNNPRKLPDYCDIPLCASS 86
DB 179 VGGPWCYTNNPRKLPDYCDVPCPSS 204
RESULT 6
AAG67228
ID AAG67228 standard; Protein; 810 AA.
XX
XX AAG67228;
XX
XX 13-NOV-2001 (first entry)
XX
XX Amino acid sequence of monkey plasminogen.
XX
XX Angiotectatin; plasminogen; sulfhydryl donor; angiogenesis; tumour;
XX angiogenic disease; neoplastic disease; connective tissue disorder;
XX rheumatoid arthritis; atherosclerosis; ocular angiogenic disease;
XX diabetic retinopathy; corneal graft rejection; cardiovascular disease;
XX cerebral vascular disease; diabetes; immune disorder;
XX chronic inflammation; autoimmunity.
XX
XX Macaca mulatta.
XX
XX WO200158921-A2.
XX
XX 16-AUG-2001.
XX
XX 08-FEB-2001, 2001WO-US04021.
XX
XX 08-FEB-2000; 2000US-0500397.
XX
XX (NOUN) UNIV NORTHWESTERN.
XX
XX Soff G, Gately ST, Twardowski P;
XX WPI, 2001-550019/61.
XX
XX Producing angiotectatin for treating angiogenic diseases involves
PT contacting plasminogen with plasminogen activator and sulfhydryl donor
PT simultaneously, or producing plasmin which is contacted with sulfhydryl
XX donor
XX
XX Disclosure; Page 90-93; 101pp; English.

XX
XX The specification describes a method for generating angiotectatin in
CC vitro. The method comprises contacting plasminogen with a sulfhydryl
CC donor, or culturing cells capable of producing plasminogen activator
CC in conditioned culture medium (CCM) and contacting the CCM with
CC plasminogen. Angiotectatin produced by method of the invention is useful
CC for treating animals with angiogenesis diseases. It is useful for
CC treating an angiogenic disease such as neoplastic diseases (e.g. tumours
CC and tumour metastasis), benign tumours (e.g. hemangiomas, acoustic
CC neuromas, etc), connective tissue disorders (e.g. rheumatoid arthritis
CC and atherosclerosis), ocular angiogenic diseases (e.g. diabetic
CC retinopathy, corneal graft rejection, etc), cardiovascular diseases,
CC cerebral vascular diseases, diabetes-associated diseases and immune
CC disorders (e.g. chronic inflammation and autoimmunity). The present
CC sequence represents a plasminogen.
XX
SQ Sequence 810 AA;
Query Match 85.0%; Score 432; DB 22; Length 810;
Best Local Similarity 83.7%; Pred. No. 2.8e-34;
Matches 72; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 EDDCMFNGNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNKAGLEKXNCRNPDG 60
DB 478 EDDCMFNGNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNKAGLEKXNCRNPDG 537
QY 61 INGPWCYTNNPRKLPDYCDIPLCASS 86
DB 538 VGGPWCYTNNPRKLPDYCDVPCPSS 563
RESULT 7
AAB01914
ID AAB01914 standard; Protein; 90 AA.
XX
XX AAB01914;
XX
XX 18-SEP-2000 (first entry)
XX
XX Human plasminogen kringles 5 (Val1454-Ala1543).
XX
XX Plasminogen; human; kringles domain; endothelial cell proliferation;
XX angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
XX antipsoriatic; antiinflammatory; anticancer; antirheumatic; antiarthritic;
XX antiangiogenic; cancer; tumour; autoimmune disease.
XX
XX Homo sapiens.
XX
XX US6057122-A.
XX
XX 02-MAY-2000.
XX
XX 05-MAY-1997; 97US-0851350.
XX
XX 03-MAY-1996; 96US-0643219.
XX
XX 03-APR-1997; 97US-0832087.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Davidson DJ;
XX
XX WPI, 2000-349573/30.
XX
XX Preparation of Kringles five peptide fragment for treating various
PT disorders such as angiogenic, ocular, skin diseases and cancer.
PT involves mixing mammalian plasminogen and elastase followed by
PT incubation and isolation
XX
XX Example 17; Page -; 48pp; English.
XX
XX The invention relates to a method of preparing plasminogen kringles 5
XX peptide fragments. The method comprises mixing mammalian plasminogen and
XX elastase in the ratio 1:100-1:300, followed by incubating and isolating

SQ Sequence 90 AA;

Qy 1 E0DCMFGNGKGYRGKCAATTVTGTCQCEMAAOEPHRHSTIIPGTMKAGLEKNYCRNPDDG 600

D6 6 EEDCMFGNGKGYRGKCAATTVTGTCQDMAAOEPHRHSITPTPTNRAGLEKNYCRNPDDG 655

```

Qy      61  INGPWCYTMNPKLFDYCDIPLCAS 85
        : ||||| : ||| :
Db      66  VGGPWCYTTNPKLYDCDVPQCAA 90

```

RESULT 8
AAV58868
ID AAV58868 standard; Protein; 91 AA.

AC AAY58868;

DT 08-MAY-2000 (first entry)

Human plasminogen mature polypeptide.

KW Anti-angiogenic; angiogenesis inhibitor; cancer; tumour; therapy;

OS Homo sapiens.

PN WO200004052-A2.

PD 27-JAN-2000.

PF 16-JUL-1999; 99WO-GB02292.

PR 16-JUL-1998; 98GB-0015505.

PA (ADPR-) ADPROTECH PLC.

PI Smith RAG, Bright JR, Steward M, Cox VF;
vxy

DR WPI; 2000-182406/16.

PT New soluble derivative of anti-angiogenic polypeptide useful for treatment of primary or secondary cancers, contains covalently attached membrane-binding elements for targeting -

PS Example 3; Page 21; 36pp; English.

CC The present sequence is that of human plasminogen mature
CC polypeptide. The invention relates to new soluble derivatives (I
CC of anti-angiotensin polypeptides. (I) comprise 2 or more

SQ Sequence 91 AA;

| | | | |
|-----------------------|------------------|---------------------|-------------------|
| Query Match | 84.6% | Score 430 ; DB 21 ; | Length 91 ; |
| Best Local Similarity | 82.4% | Pred. No. 5.1e-35 ; | |
| Matches 70 ; | Conservative 7 ; | Mismatches 8 ; | Indels 0 ; Gaps 0 |

```
QY      1 EDDCNFGNGSGYRGKKAATTVTGTPCQDAQAQEPHRHSTFIPTGNMKAGLEKNYCRRPDDG    60
        :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      2 EEDCNFNGNGSGYRGKKAATTVTGTPCQDAQAQEPHRHSIPTPETPRAGLEKNYCRRPDDG    61
```

```

Oy      61  INGPWCYTNPRKLFDYCDIPLCAS 85
          : ||||| ||||: |||:
Db      62  VGGFWCYTNPRKLYDYCDVPQCAA 86

```

RESULT 9
AAB01917
ID AAB01917 standard; Protein; 93 AA

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringler 5 (Val1454-Phe546).
DE

KW Plasminogen; human; endothelial cell proliferation

KW anti-psoriatic; anti-inflammatory; anti-ulcer; anti-rheumatic; anti-arthritic; anti-oncogenic; cancer; tumour; autoimmune disease

Homocysteine

XX PN TS6057122-A

XX
PD 03-MAY-2000

XX 05-MAY-1997: 97US-0851350.
PF

XX
PR 03-MAY-1996: 96US-0643219.

PK 03-APR-1997; 9705-0832087.
XX

PA (ABBU / ABBOLI LAB
XX

PL DAVLAB011 DO NOT
XXX

DR MFL; 2000-3495/3/30-
XX

PT Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -

PS Example 17; Page -; 48pp; English.

The invention relates to a method of preparing lamininogen kringle 5 peptide fragments. The method comprises mixing mammalian lamininogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract,

CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
 CC syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
 CC in an exemplification of the invention.
 CC Note: This sequence is not shown in the specification, but is derived
 CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.

XX Sequence 93 AA;

SO Query Match 84.6%; Score 430; DB 21; Length 93;

Best Local Similarity 82.4%; Pred. No. 5.3e-35;
 Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSITPTNNKAGLEKXNCRNPDGD 60
 Db 6 EDDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSITPTNNKAGLEKXNCRNPDGD 65

QY 61 INGPWCYTNNPRKLFYCDIPLCAS 85
 Db 66 VGSPWCYTNNPRKLYDCVPCQAA 90

RESULT 10

AAB01913
 ID AAB01913 standard; Protein; 95 AA.

XX AAB01913;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringle 5 (Val1449-Ala543).

XX Plasminogen; human; kringle domain; endothelial cell proliferation;
 KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
 KM antipsoietic; antiinflammatory; antitumor; antirheumatic; antiarthritic;
 KM antiangiogenic; cancer; tumour; autoimmune disease.

XX Homo sapiens.

OS US6057122-A.

PN 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

XX 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

XX (ABBO) ABBOTT LAB.

PI Davidson DJ;

DR WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various
 PT disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -

XX Example 17; Page -; 48pp; English.

CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating

CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
 CC syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
 CC in an exemplification of the invention.
 CC Note: This sequence is not shown in the specification, but is derived
 CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.

XX Sequence 95 AA;

SO Query Match 84.6%; Score 430; DB 21; Length 95;

Best Local Similarity 82.4%; Pred. No. 5.4e-35;
 Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSITPTNNKAGLEKXNCRNPDGD 60
 Db 11 EDDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSITPTNNKAGLEKXNCRNPDGD 70

QY 61 INGPWCYTNNPRKLFYCDIPLCAS 85
 Db 71 VGSPWCYTNNPRKLYDCVPCQAA 95

RESULT 11

AAB01916
 ID AAB01916 standard; Protein; 98 AA.

XX AAB01916;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringle 5 (Val1449-Phe546).

XX Plasminogen; human; kringle domain; endothelial cell proliferation;
 KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
 KM antipsoietic; antiinflammatory; antitumor; antirheumatic; antiarthritic;
 KM antiangiogenic; cancer; tumour; autoimmune disease.

XX Homo sapiens.

OS US6057122-A.

PN 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

XX 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

XX (ABBO) ABBOTT LAB.

PI Davidson DJ;

DR WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various
 PT disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -

XX Example 17; Page -; 48pp; English.

XX Preparation of Kringle five peptide fragment for treating various
PT disorders such as angiogenic, ocular, skin diseases and cancer,
PT involves mixing mammalian plasminogen and elastase followed by
PT incubation and isolation -

PS Disclosure; Fig 2; 48pp; English.

CC The invention relates to a method of preparing plasminogen kringles 5
CC and peptide fragments. The method comprises mixing mammalian plasminogen and
CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
CC the fragment. The kringles 5 peptides are inhibitors of angiogenesis and
CC endothelial cell proliferation and migration. The peptides are useful
CC for treating angiogenic diseases, primary and metastatic solid tumours
CC and carcinomas of various organs such as breast, genital tract,
CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
CC arising from hematopoietic malignancies such as leukaemias and
CC lymphomas. They are also used for the prophylaxis of various autoimmune
CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
CC (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
CC Syndrome), diseases caused by excessive or abnormal stimulation of
CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
CC disease and ulcers). The peptides are also useful as a birth control
CC agent which inhibits ovulation and establishment of the placenta.
CC Sequences AAB01890-801894 represent, respectively, human, murine, Rhesus
CC monkey, bovine and porcine plasminogen kringles 5 domains.

XX Sequence 101 AA;

Query Match 84.6%; Score 430; DB 21; Length 101;
Best Local Similarity 82.4%; Pred. No. 5, 7e-35;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDCMFNGNGKGYRGKATVTGTPCEMAAOEPHRSITPTGNTKAGLEKNTCRNPDG 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 17 EEDCMFNGNGKGYRGKATVTGTPCEMAAOEPHRSITPTGNTKAGLEKNTCRNPDG 76

QY 61 INGPWCYTNNPKLFYDCDIPLCAS 85
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 77 VGGPWCYTNNPKLYDCDVPQCAA 101

RESULT 14

AAB01912 standard; Protein; 101 AA.

AC AAB01912;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringles 5 (Val1443-Ala543).

XX Plasminogen; human; kringle domain; endothelial cell proliferation;
XX angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
KW antiproliferative; antiinflammatory; anticancer; antineoplastic;
KW antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

PR 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

XX (ABBO) ABBOTT LAB.

PA Davidson DJ;

XX

DR WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various
PT disorders such as angiogenic, ocular, skin diseases and cancer,
PT involves mixing mammalian plasminogen and elastase followed by
PT incubation and isolation -

XX Example 17; Page -; 48pp; English.

CC The invention relates to a method of preparing plasminogen kringles 5
CC and peptide fragments. The method comprises mixing mammalian plasminogen and
CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
CC the fragment. The kringles 5 peptides are inhibitors of angiogenesis and
CC endothelial cell proliferation and migration. The peptides are useful
CC for treating angiogenic diseases, primary and metastatic solid tumours
CC and carcinomas of various organs such as breast, genital tract,
CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
CC arising from hematopoietic malignancies such as leukaemias and
CC lymphomas. They are also used for the prophylaxis of various autoimmune
CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
CC (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
CC Syndrome), diseases caused by excessive or abnormal stimulation of
CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
CC disease and ulcers). The peptides are also useful as a birth control
CC agent which inhibits ovulation and establishment of the placenta.
CC Sequences AAB01906-801919 represent fragments of human plasminogen used
CC in an exemplification of the invention.

CC Note: This sequence is not shown in the specification, but is derived
CC from the full length human plasminogen sequence (AAB01887) shown in
CC figure 1.

SO Sequence 101 AA;

Query Match 84.6%; Score 430; DB 21; Length 101;
Best Local Similarity 82.4%; Pred. No. 5, 7e-35;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDCMFNGNGKGYRGKATVTGTPCEMAAOEPHRSITPTGNTKAGLEKNTCRNPDG 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 17 EEDCMFNGNGKGYRGKATVTGTPCEMAAOEPHRSITPTGNTKAGLEKNTCRNPDG 76

QY 61 INGPWCYTNNPKLFYDCDIPLCAS 85
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 77 VGGPWCYTNNPKLYDCDVPQCAA 101

RESULT 15

AAB01915 standard; Protein; 104 AA.

AC AAB01915;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringles 5 (Val1443-Phe546).

XX Plasminogen; human; kringle domain; endothelial cell proliferation;
XX angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
KW antiproliferative; antiinflammatory; anticancer; antineoplastic;
KW antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

PR 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

XX

PA (ABBO) ABBOTT LAB.

PI Davidson DJ;

WPI; 2000-349573/30.

PT Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, PT involves mixing mammalian plasminogen and elastase followed by incubation and isolation -

PS Example 17; Page -; 48pp; English.

The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01906-B01919 represent fragments of human plasminogen used in an exemplification of the invention.

Note: This sequence is not shown in the specification, but is derived from the full length human plasminogen sequence (AAB01867) shown in figure 1.

| | | | | |
|-------------|--------|------------|--------|-------------|
| Query Match | 84.6%; | Score 430; | DB 21; | Length 104; |
|-------------|--------|------------|--------|-------------|

| | | | | | | | | | |
|---------|-----|--------------|----|------------|----|--------|----|------|----|
| Matches | 70; | Conservative | 7; | Mismatches | 8; | Indels | 0; | Gaps | 0; |
|---------|-----|--------------|----|------------|----|--------|----|------|----|

[illegible]

61 INGPWCYTNNPRKLFYDCDIPLCAS 85

Db 77 VGGPWCYTTNPRKLYDYCDVPQCAA 101

Search completed: January 12, 2004, 17:23:22
Job time : 35.2707 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 17:24:03 ; Search time 25.218 Seconds
(without alignments)
687.200 Million cell updates/sec

Title: US-10-088-548-8

Perfect score: 508
Sequence: 1 EODCMFGNGKGRGKATTV.....YTMNPRKLFYCDIPLCASS 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|------|---|
| 1 | 508 | 100.0 | 91 | US-09-748-468-1 Sequence 1, Appli |
| 2 | 508 | 100.0 | 1169 | US-09-870-759-126 Sequence 126, App |
| 3 | 508 | 100.0 | 1169 | US-09-751-708A-126 Sequence 126, App |
| 4 | 430 | 84.6 | 791 | US-09-967-386-1 Sequence 1, Appli |
| 5 | 430 | 84.6 | 791 | US-10-304-287-1 Sequence 1, Appli |
| 6 | 430 | 84.6 | 810 | US-09-946-893-2 Sequence 2, Appli |
| 7 | 430 | 84.6 | 810 | US-10-193-144-1 Sequence 1, Appli |
| 8 | 430 | 84.6 | 810 | US-10-237-656-2 Sequence 1, Appli |
| 9 | 427 | 84.1 | 569 | US-09-946-893-5 Sequence 5, Appli |
| 10 | 427 | 84.1 | 571 | US-09-946-893-8 Sequence 8, Appli |
| 11 | 427 | 84.1 | 576 | US-09-946-893-6 Sequence 6, Appli |
| 12 | 425 | 83.7 | 458 | US-09-946-893-4 Sequence 4, Appli |
| 13 | 412 | 81.1 | 80 | US-09-753-064-6 Sequence 6, Appli |
| 14 | 412 | 81.1 | 80 | US-10-267-137-8 Sequence 8, Appli |
| 15 | 406 | 79.9 | 812 | US-09-788-142-1 Sequence 1, Appli |

| | | | | | | |
|----|-------|------|-----|----|--------------------|--------------------|
| 16 | 406 | 79.9 | 812 | 9 | US-09-761-120-1 | Sequence 1, Appli |
| 17 | 406 | 79.9 | 812 | 9 | US-09-873-676-81 | Sequence 81, Appli |
| 18 | 406 | 79.9 | 812 | 10 | US-09-335-125-1 | Sequence 1, Appli |
| 19 | 406 | 79.9 | 812 | 12 | US-10-402-364-1 | Sequence 1, Appli |
| 20 | 406 | 79.9 | 812 | 15 | US-10-131-241-1 | Sequence 1, Appli |
| 21 | 405 | 79.7 | 79 | 9 | US-09-753-064-1 | Sequence 1, Appli |
| 22 | 397 | 78.1 | 459 | 9 | US-09-761-120-46 | Sequence 46, Appli |
| 23 | 397 | 78.1 | 459 | 12 | US-10-402-364-46 | Sequence 46, Appli |
| 24 | 387 | 76.2 | 80 | 9 | US-09-761-120-47 | Sequence 47, Appli |
| 25 | 387 | 76.2 | 80 | 12 | US-10-402-364-47 | Sequence 47, Appli |
| 26 | 276.5 | 54.4 | 339 | 9 | US-09-788-142-4 | Sequence 4, Appli |
| 27 | 276.5 | 54.4 | 339 | 9 | US-09-761-120-4 | Sequence 4, Appli |
| 28 | 276.5 | 54.4 | 339 | 9 | US-09-335-125-4 | Sequence 4, Appli |
| 29 | 276.5 | 54.4 | 339 | 12 | US-10-402-364-4 | Sequence 4, Appli |
| 30 | 276.5 | 54.4 | 339 | 15 | US-10-131-241-4 | Sequence 4, Appli |
| 31 | 274.5 | 54.0 | 79 | 9 | US-09-761-120-9 | Sequence 9, Appli |
| 32 | 274.5 | 54.0 | 79 | 10 | US-09-335-125-9 | Sequence 9, Appli |
| 33 | 274.5 | 54.0 | 79 | 12 | US-10-402-364-9 | Sequence 9, Appli |
| 34 | 274.5 | 54.0 | 79 | 15 | US-10-131-241-9 | Sequence 9, Appli |
| 35 | 274.5 | 54.0 | 160 | 9 | US-09-761-120-36 | Sequence 36, Appli |
| 36 | 274.5 | 54.0 | 160 | 10 | US-09-335-125-36 | Sequence 36, Appli |
| 37 | 274.5 | 54.0 | 160 | 12 | US-10-402-364-36 | Sequence 36, Appli |
| 38 | 274.5 | 54.0 | 160 | 15 | US-10-131-241-36 | Sequence 36, Appli |
| 39 | 274.5 | 54.0 | 250 | 9 | US-09-761-120-31 | Sequence 31, Appli |
| 40 | 274.5 | 54.0 | 250 | 10 | US-09-335-125-31 | Sequence 31, Appli |
| 41 | 274.5 | 54.0 | 250 | 12 | US-10-402-364-31 | Sequence 31, Appli |
| 42 | 274.5 | 54.0 | 250 | 15 | US-10-131-241-31 | Sequence 31, Appli |
| 43 | 272.5 | 53.6 | 83 | 12 | US-09-981-151A-86 | Sequence 86, Appli |
| 44 | 269.5 | 53.1 | 81 | 12 | US-10-004-578A-188 | Sequence 188, App |
| 45 | 267.5 | 52.7 | 79 | 12 | US-09-981-151A-85 | Sequence 85, Appli |

ALIGNMENTS

RESULT 1
US-09-748-468-1
; Sequence 1, Application US/09748468
; Patent No. US20010051347A1
; GENERAL INFORMATION:
; APPLICANT: Kundu, S.
; TITLE OF INVENTION: SPECIFIC ANTIBODIES TO KRINGLE 5 OF
; TITLE OF INVENTION: APO(A) AND METHODS OF USE THEREFOR
; FILE REFERENCE: 6296 US. 01
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: 09/234,553
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-468-1

Query Match 100.0%; Score 508; DB 9; Length 91;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 61 INGPWCYTMNPRKLFYCDIPLCASS 86
3 EODCMFGNGKGRGKATTVGTGTCQEAADPHSHSTIFGTINWAGLEKNYCNPPGD 62
63 INGPWCYTMNPRKLFYCDIPLCASS 88
RESULT 2
US-09-870-759-126
; Sequence 126, Application US/09870759

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; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 126
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-870-759-126

Query Match      100.0%; Score 508; DB 10; Length 1169;
Best Local Similarity 100.0%; Pred. No. 3,1e-48;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EODCMFNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNKMAGLEKNTCRNPDGD 60
Db 846 EODCMFNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNKMAGLEKNTCRNPDGD 905

Qy 61 INGPWCYTNNPRKLFYCDIPLCASS 86
Db 906 INGPWCYTNNPRKLFYCDIPLCASS 931

RESULT 3
; US-09-751-708A-126
; Sequence 126, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 126
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-751-708A-126

Query Match      100.0%; Score 508; DB 12; Length 1169;
Best Local Similarity 100.0%; Pred. No. 3,1e-48;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EODCMFNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNKMAGLEKNTCRNPDGD 60
Db 846 EODCMFNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNKMAGLEKNTCRNPDGD 905

Qy 61 INGPWCYTNNPRKLFYCDIPLCASS 86
Db 906 INGPWCYTNNPRKLFYCDIPLCASS 931

RESULT 4
; US-09-967-386-1
; Sequence 1, Application US/09967386
; Patent No. US20020159992A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Henkin, Jack
; APPLICANT: Davidson, Donald J.
; TITLE OF INVENTION: ANTIANGIOGENIC POLYPEPTIDES AND METHODS
; TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
```

```
; FILE REFERENCE: 6738.US.02
; CURRENT APPLICATION NUMBER: US/09/967,386
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/236,550
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-967-386-1

Query Match      84.6%; Score 430; DB 10; Length 791;
Best Local Similarity 82.4%; Pred. No. 1,1e-39;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EODCMFNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNKMAGLEKNTCRNPDGD 60
Db 459 EODCMFNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNPRAGLEKNTCRNPDGD 518

Qy 61 INGPWCYTNNPRKLFYCDIPLCASS 85
Db 519 VGSPWCYTNNPRKLYDYCDVPCAA 543

RESULT 5
; US-10-304-287-1
; Sequence 1, Application US/10304287
; Publication No. US20030083234A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, MiJung
; APPLICANT: Waisman, David M.
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; FILE REFERENCE: ME02-001
; CURRENT APPLICATION NUMBER: US/10/304,287
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/333,866
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 791
; TYPE: PRT
; ORGANISM: mammalian
; US-10-304-287-1

Query Match      84.6%; Score 430; DB 15; Length 791;
Best Local Similarity 82.4%; Pred. No. 1,1e-39;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EODCMFNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNKMAGLEKNTCRNPDGD 60
Db 459 EODCMFNGKGYRGKATTTGTGTCQEWAAQEPHRSHTFPGTNPRAGLEKNTCRNPDGD 518

Qy 61 INGPWCYTNNPRKLFYCDIPLCASS 85
Db 519 VGSPWCYTNNPRKLYDYCDVPCAA 543

RESULT 6
; US-09-946-893-2
; Sequence 2, Application US/09946893
; Patent No. US20020072494A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Inhibitors
; CURRENT APPLICATION NUMBER: US/09/946,893
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
```

NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 810
TYPE: PRT
ORGANISM: Homo sapiens
US-09-946-893-2

Query Match 84.6%; Score 430; DB 9; Length 810;
Best Local Similarity 82.4%; Pred. No. 1,2e-39;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSIFPGTNKAGLEKXNCRNPDG 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 478 EDDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSIFPGTNKAGLEKXNCRNPDG 537
QY 61 INGPWCYTMNPRKLFYCDIPLCAS 85
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 538 VGGPWCYTMNPRKLYDCVPOCAA 562

RESULT 7

US-10-237-144-1
Sequence 1, Application US/10237144
Publication No. US20030147879A1
GENERAL INFORMATION:
APPLICANT: NY, Tor
APPLICANT: LI, Jinnan
APPLICANT: HELSTROM, Sten
APPLICANT: ERIKSSON, Per-Olof
TITLE OF INVENTION: METHOD OF WOUND HEALING
FILE REFERENCES: 3810/11759-US1
CURRENT APPLICATION NUMBER: US/10/237,144
CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/317,643
PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 810
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / 625234
DATABASE ENTRY DATE: 2000-09-15
RELEVANT RESIDUES: (1)..(810)
US-10-237-144-1

Query Match 84.6%; Score 430; DB 12; Length 810;
Best Local Similarity 82.4%; Pred. No. 1,2e-39;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSIFPGTNKAGLEKXNCRNPDG 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 478 EDDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSIFPGTNKAGLEKXNCRNPDG 537
QY 61 INGPWCYTMNPRKLFYCDIPLCAS 85
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 538 VGGPWCYTMNPRKLYDCVPOCAA 562

RESULT 8

US-10-193-656-2
Sequence 2, Application US/10193656
Publication No. US20030096733A1
GENERAL INFORMATION:
APPLICANT: NY, Tor
APPLICANT: HOLMDAHL, Rikard
APPLICANT: LI, Jinnan
TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
FILE REFERENCES: 3810/11577-US3
CURRENT APPLICATION NUMBER: US/10/193,656
CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US 60/304,461
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/304,490
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/305,182
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 810
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P00747
DATABASE ENTRY DATE: 1986-07-21
RELEVANT RESIDUES: (1)..(810)
US-10-193-656-2

Query Match 84.6%; Score 430; DB 15; Length 810;
Best Local Similarity 82.4%; Pred. No. 1,2e-39;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSIFPGTNKAGLEKXNCRNPDG 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 478 EDDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSIFPGTNKAGLEKXNCRNPDG 537
QY 61 INGPWCYTMNPRKLFYCDIPLCAS 85
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 538 VGGPWCYTMNPRKLYDCVPOCAA 562

RESULT 9

US-09-946-893-5
Sequence 5, Application US/09946893
Patent No. US20020072494A1
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
FILE REFERENCES: Newburn
CURRENT APPLICATION NUMBER: US/09/946,893
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/230,893
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 569
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
US-09-946-893-5

Query Match 84.1%; Score 427; DB 9; Length 569;
Best Local Similarity 80.2%; Pred. No. 1,7e-39;
Matches 69; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSIFPGTNKAGLEKXNCRNPDG 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 478 EDDCMFGNGKGYRGKATTTGTGTCQEWAAQEPHRSIFPGTNKAGLEKXNCRNPDG 537
QY 61 INGPWCYTMNPRKLFYCDIPLCAS 86
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 538 VGGPWCYTMNPRKLYDCVPOCAA 563

RESULT 10

US-09-946-893-8
Sequence 8, Application US/09946893
Patent No. US20020072494A1
GENERAL INFORMATION:
APPLICANT: Cao, Yihai

```

; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Newburn
; CURRENT APPLICATION NUMBER: US/09/946,893
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
; OTHER INFORMATION: with a tumor targeting signal peptide
; US-09-946-893-8

Query Match      84.1%; Score 427; DB 9; Length 571;
Best Local Similarity 80.2%; Pred. No. 1.7e-39;
Matches 69; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATVTGTPCOEWAAQEPHRSHTPIPGTNKWALEKXNCRNPDG 60
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 EEDCMFGNGKGYRGKATVTGTPCOEWAAQEPHRSHTPIPETNPRAGLEKXNCRNPDG 537
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 INGPWCYTNNPRKLFYDCDIPLCASS 86
    :|||||:|||||:|||||:|||||:
Db 538 VGGPMCTTNNPRKLYDYCDVPOCCAA 563
    :|||||:|||||:|||||:|||||:

RESULT 11
; Sequence 6, Application US/09946893
; Patent No. US20020072494A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Newburn
; CURRENT APPLICATION NUMBER: US/09/946,893
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Angiogenesis
; OTHER INFORMATION: with a tumor targeting signal
; US-09-946-893-6

Query Match      84.1%; Score 427; DB 9; Length 576;
Best Local Similarity 80.2%; Pred. No. 1.7e-39;
Matches 69; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATVTGTPCOEWAAQEPHRSHTPIPGTNKWALEKXNCRNPDG 60
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 EEDCMFGNGKGYRGKATVTGTPCOEWAAQEPHRSHTPIPETNPRAGLEKXNCRNPDG 537
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 INGPWCYTNNPRKLFYDCDIPLCASS 86
    :|||||:|||||:|||||:|||||:
Db 538 VGGPMCTTNNPRKLYDYCDVPOCCAA 563
    :|||||:|||||:|||||:|||||:

RESULT 12
; Sequence 4, Application US/09946893
; Patent No. US20020072494A1
; GENERAL INFORMATION:

; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
; FILE REFERENCE: Newburn
; CURRENT APPLICATION NUMBER: US/09/946,893
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,893
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-946-893-4

Query Match      83.7%; Score 425; DB 9; Length 458;
Best Local Similarity 83.1%; Pred. No. 2.3e-39;
Matches 69; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 EODCMFGNGKGYRGKATVTGTPCOEWAAQEPHRSHTPIPGTNKWALEKXNCRNPDG 60
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 376 EEDCMFGNGKGYRGKATVTGTPCOEWAAQEPHRSHTPIPETNPRAGLEKXNCRNPDG 435
    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 INGPWCYTNNPRKLFYDCDIPLC 83
    :|||||:|||||:|||||:|||||:
Db 436 VGGPMCTTNNPRKLYDYCDVPOC 458
    :|||||:|||||:|||||:|||||:

RESULT 13
; Sequence 6, Application US/09753064
; Patent No. US2001001644A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yihai
; TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/753,064
; FILING DATE: 29-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/763,528
; FILING DATE: 12-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714
; REFERENCE/DOCKET NUMBER: 05940-0251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
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ANTI-SENSE: NO
FRAGMENT TYPE: Internal
FEATURES:
NAME/KEY: Protein
LOCATION: 1..80
OTHER INFORMATION: /note= "Kringles 5 - Figure 3"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-753-064-6

Query Match 81.1%; Score 412; DB 9; Length 80;
Best Local Similarity 83.8%; Pred. No. 9.8e-39;
Matches 67; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 4 CMFGNGKGYRGKATVTGTPCOEWAQEPHRSSTFIPGNTKMAGLEKXKNCNPDGDDING 63
Db 1 CMFGNGKGYRGKATVTGTPCOEWAQEPHRSSTFIPGNTKMAGLEKXKNCNPDGDDING 60
Qy 64 PMCYTNMPKRLFDYCDIPLC 83
Db 61 PMCYTNMPKRLYDYCDVPOC 80

RESULT 14
US-10-267-137-8
Sequence 8, Application US/10267137
Publication No. US20030148950A1
GENERAL INFORMATION:
APPLICANT: Xian, Li
APPLICANT: Li, Zai-Ping
APPLICANT: Gan, Ren-bao
APPLICANT: Zhou, Qing-wei
APPLICANT: Xu, Ren
TITLE OF INVENTION: KRINGLE DOMAIN 1 OF HUMAN HEPATOCTE
FILE REFERENCE: 524282000100
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 80
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Sequence alignment of kringle domains of
US-10-267-137-8

Query Match 81.1%; Score 412; DB 12; Length 80;
Best Local Similarity 83.8%; Pred. No. 9.8e-39;
Matches 67; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 4 CMFGNGKGYRGKATVTGTPCOEWAQEPHRSSTFIPGNTKMAGLEKXKNCNPDGDDING 63
Db 1 CMFGNGKGYRGKATVTGTPCOEWAQEPHRSSTFIPGNTKMAGLEKXKNCNPDGDDING 60
Qy 64 PMCYTNMPKRLFDYCDIPLC 83
Db 61 PMCYTNMPKRLYDYCDVPOC 80

RESULT 15
US-09-788-142-1
Sequence 1, Application US/09788142
Patent No. US20010023246A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Akeew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 16-Feb-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/866,735
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Murine
IMMEDIATE SOURCE:
CLONE: Plasmidogen
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-788-142-1

Query Match 79.9%; Score 406; DB 9; Length 812;
Best Local Similarity 79.1%; Pred. No. 5.7e-37;
Matches 68; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 1 EDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSSTFIPGNTKMAGLEKXKNCNPDGDDING 60
Db 478 ETDGNGKGYRGKATVTGTPCOEWAQEPHRSSTFIPGNTKMAGLEKXKNCNPDGDDING 537
Qy 61 INGPWCYTNPRLFDYCDIPLC 86
Db 538 VNGPWCYTNPRLYDYCDIPLC 86

Search completed: January 12, 2004, 17:29:39
Job time : 25.218 secs

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OM protein - protein search, using sw model

Run on: January 12, 2004, 17:21:34 ; Search time 12.2857 Seconds
(without alignments)
296.176 Million cell updates/sec

Title: US-10-088-548-8

Perfect score: 508
Sequence: 1 EDDCMFGNGKGYRGKATTV.....YTMNPKLFYDCDIPCLASS 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*
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3: /cgn2_6/prodata/1/1aa/RA_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|-------------------|--------------------|
| 1 | 508 | 100.0 | 91 | 3 | US-09-234-553-1 | Sequence 1, Appli |
| 2 | 432 | 85.0 | 810 | 4 | US-08-991-761A-11 | Sequence 11, Appli |
| 3 | 430 | 84.6 | 90 | 2 | US-09-131-995-4 | Sequence 4, Appli |
| 4 | 430 | 84.6 | 90 | 2 | US-08-832-087B-4 | Sequence 4, Appli |
| 5 | 430 | 84.6 | 90 | 3 | US-09-132-154-4 | Sequence 4, Appli |
| 6 | 430 | 84.6 | 93 | 2 | US-09-131-995-7 | Sequence 7, Appli |
| 7 | 430 | 84.6 | 93 | 2 | US-08-832-087B-7 | Sequence 7, Appli |
| 8 | 430 | 84.6 | 93 | 3 | US-09-132-154-7 | Sequence 7, Appli |
| 9 | 430 | 84.6 | 95 | 2 | US-09-131-995-3 | Sequence 3, Appli |
| 10 | 430 | 84.6 | 95 | 2 | US-08-832-087B-3 | Sequence 3, Appli |
| 11 | 430 | 84.6 | 95 | 3 | US-09-132-154-3 | Sequence 3, Appli |
| 12 | 430 | 84.6 | 98 | 2 | US-09-131-995-6 | Sequence 6, Appli |
| 13 | 430 | 84.6 | 98 | 2 | US-08-832-087B-6 | Sequence 6, Appli |
| 14 | 430 | 84.6 | 98 | 3 | US-09-132-154-6 | Sequence 6, Appli |
| 15 | 430 | 84.6 | 101 | 2 | US-09-131-995-2 | Sequence 2, Appli |
| 16 | 430 | 84.6 | 101 | 2 | US-08-832-087B-2 | Sequence 2, Appli |
| 17 | 430 | 84.6 | 101 | 3 | US-08-851-350-34 | Sequence 34, Appli |
| 18 | 430 | 84.6 | 101 | 3 | US-09-132-154-2 | Sequence 2, Appli |
| 19 | 430 | 84.6 | 104 | 2 | US-09-131-995-5 | Sequence 5, Appli |
| 20 | 430 | 84.6 | 104 | 2 | US-08-832-087B-5 | Sequence 5, Appli |
| 21 | 430 | 84.6 | 104 | 3 | US-09-132-154-5 | Sequence 5, Appli |
| 22 | 430 | 84.6 | 790 | 1 | US-08-469-486-54 | Sequence 54, Appli |
| 23 | 430 | 84.6 | 790 | 2 | US-08-469-658-54 | Sequence 54, Appli |
| 24 | 430 | 84.6 | 791 | 2 | US-09-131-995-1 | Sequence 1, Appli |
| 25 | 430 | 84.6 | 791 | 2 | US-08-832-087B-1 | Sequence 1, Appli |
| 26 | 430 | 84.6 | 791 | 3 | US-09-132-154-1 | Sequence 1, Appli |
| 27 | 430 | 84.6 | 791 | 4 | US-08-991-761A-6 | Sequence 6, Appli |

| | | | | | | |
|----|-----|------|-----|---|-------------------|--------------------|
| 28 | 430 | 84.6 | 810 | 1 | US-07-854-603-2 | Sequence 2, Appli |
| 29 | 430 | 84.6 | 810 | 1 | US-08-147-000B-29 | Sequence 29, Appli |
| 30 | 430 | 84.6 | 810 | 3 | US-09-086-514-1 | Sequence 1, Appli |
| 31 | 430 | 84.6 | 810 | 4 | US-09-192-012-5 | Sequence 5, Appli |
| 32 | 430 | 84.6 | 810 | 6 | 5200340-8 | Patent No. 5200340 |
| 33 | 430 | 84.6 | 814 | 1 | US-08-750-711-1 | Sequence 1, Appli |
| 34 | 428 | 84.3 | 101 | 3 | US-08-851-350-36 | Sequence 36, Appli |
| 35 | 425 | 83.7 | 90 | 1 | US-08-643-219-4 | Sequence 4, Appli |
| 36 | 425 | 83.7 | 93 | 1 | US-08-643-219-7 | Sequence 7, Appli |
| 37 | 425 | 83.7 | 95 | 1 | US-08-643-219-3 | Sequence 3, Appli |
| 38 | 425 | 83.7 | 98 | 1 | US-08-643-219-6 | Sequence 6, Appli |
| 39 | 425 | 83.7 | 101 | 1 | US-08-643-219-2 | Sequence 2, Appli |
| 40 | 425 | 83.7 | 104 | 1 | US-08-643-219-5 | Sequence 5, Appli |
| 41 | 425 | 83.7 | 333 | 4 | US-08-991-761A-8 | Sequence 8, Appli |
| 42 | 425 | 83.7 | 791 | 3 | US-08-643-219-1 | Sequence 1, Appli |
| 43 | 425 | 83.7 | 791 | 3 | US-08-851-350-1 | Sequence 1, Appli |
| 44 | 419 | 82.5 | 100 | 1 | US-08-643-219-9 | Sequence 9, Appli |
| 45 | 419 | 82.5 | 100 | 2 | US-09-131-995-9 | Sequence 9, Appli |

ALIGNMENTS

```
RESULT 1
US-09-234-553-1
; Sequence 1, Application US/09234553
; Patent No. 6210906
; GENERAL INFORMATION:
; APPLICANT: Kundu, S.
; TITLE OF INVENTION: SPECIFIC ANTIBODIES TO KRINGLE 5 OF
; FILE REFERENCE: 6296 US 01
; CURRENT APPLICATION NUMBER: US/09/234.553
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-234-553-1

Query Match      100.0%; Score 508; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. NO. 1.3e-50;
Matches      86; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 EDDCMFGNGKGYRGKATTVTGTGTCQEWAAOEPHRSHTFIPGTNKMAGLEKNYCRNPDGD 60
DB      3 EDDCMFGNGKGYRGKATTVTGTGTCQEWAAOEPHRSHTFIPGTNKMAGLEKNYCRNPDGD 62
QY      61 INGPWCYTMNPKLFYDCDIPCLASS 86
DB      63 INGPWCYTMNPKLFYDCDIPCLASS 88

RESULT 2
US-08-991-761A-11
; Sequence 11, Application US/08991761A
; Patent No. 6576609
; GENERAL INFORMATION:
; APPLICANT: Seff, Gerald
; APPLICANT: Gately, Stephen
; APPLICANT: Twardowski, Przemyslaw
; TITLE OF INVENTION: "Methods and Compositions for Generating
; TITLE OF INVENTION: "Methods and Compositions for Generating
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sheridan Rose P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
```

```

:
: ZIP: 80203
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/991,761A
: FILING DATE:
: CLASSIFICATION: 1642
: ATTORNEY/AGENT INFORMATION:
: NAME: Crook, Wanneil M.
: REGISTRATION NUMBER: 31,071
: REFERENCE//DOCKET NUMBER: 3501-16-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 863-9700
: TELEFAX: (303) 863-0223
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 810 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-991-761A-11

Query Match      85.0%; Score 432; DB 4; Length 810;
Best Local Similarity 83.7%; Pred. No. 6.8e-41;
Matches 72; Conservative 4; Mismatches 10; Gaps 0;

QY 1 EODCMFNGKGYRGKATVTGTPCQEWAAQEPHRSTFPGTNKAGLEKNCRNPDGD 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 EEDCMFNGKGYRGKATVTGTPCQEWAAQEPHRSHIFPETNPAGLEKNCRNPDGD 537
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 INGPWCYTNPRLPYCDIPLCAS 86
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 538 VGGPWCYTNPRLPYCDVPOCAAS 563
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
US-09-131-995-4
: Sequence 4, Application US/09131995
: Patent No. 5972896
: GENERAL INFORMATION:
: APPLICANT: Davidson, Donald J.
: TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
: TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Abbott Laboratories
: STREET: 100 Abbott Park Road
: CITY: Abbott Park
: STATE: IL
: COUNTRY: USA
: ZIP: 60064
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/131,995
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/832,087
: FILING DATE: 03-APR-1997
: APPLICATION NUMBER: 08/643,219
: FILING DATE: 06-MAY-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Casuto, Dianne
: REGISTRATION NUMBER: 40,943
: REFERENCE//DOCKET NUMBER: 5940-US.P1
: REFERENCE//DOCKET NUMBER: 5940-US.P1
```

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:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 847-938-3137
: TELEFAX: 847-938-2623
: TELEX:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 90 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE:
: DESCRIPTION: protein
: FRAGMENT TYPE: internal
: US-09-131-995-4

Query Match      84.6%; Score 430; DB 2; Length 90;
Best Local Similarity 82.4%; Pred. No. 9.6e-42;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EODCMFNGKGYRGKATVTGTPCQEWAAQEPHRSTFPGTNKAGLEKNCRNPDGD 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 EEDCMFNGKGYRGKATVTGTPCQEWAAQEPHRSHIFPETNPAGLEKNCRNPDGD 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 INGPWCYTNPRLPYCDIPLCAS 85
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 VGGPWCYTNPRLPYCDVPOCAA 90
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-08-832-087B-4
: Sequence 4, Application US/08832087B
: Patent No. 5981484
: GENERAL INFORMATION:
: APPLICANT: Davidson, Donald J.
: TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
: TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Abbott Laboratories
: STREET: 100 Abbott Park Road
: CITY: Abbott Park
: STATE: IL
: COUNTRY: USA
: ZIP: 60064
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/832,087B
: FILING DATE: 03-APR-1997
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/643,219
: FILING DATE: 06-MAY-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Casuto, Dianne
: REGISTRATION NUMBER: 40,943
: REFERENCE//DOCKET NUMBER: 5940-US.P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 847-938-3137
: TELEFAX: 847-938-2623
: TELEX:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 90 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: DESCRIPTION: protein
: FRAGMENT TYPE: internal
: US-08-832-087B-4
```

Query Match 84.6%; Score 430; DB 2; Length 90;
Best Local Similarity 82.4%; Pred. No. 9.6e-42;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSSTFTPTNKAGLEKXKNCNPDG 60
DB 6 EEDCMFGNGKGYRGKATVTGTPCODMAQEPHRSSTFTPTNPAAGLEKXKNCNPDG 65
QY 61 INGPWCYTNNPRKLFYCDIPICAS 85
DB 66 VGGPWCYTNNPRKLYDYCDVPQCA 90

RESULT 5
US-09-132-154-4
Sequence 4, Application US/09122154
Patent No. 6251867

GENERAL INFORMATION:

APPLICANT: Davidson, Donald J.

TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/132,154

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/832,087

FILING DATE: 03-APR-1997

APPLICATION NUMBER: 08/643,219

FILING DATE: 06-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Casuto, Dianne

REGISTRATION NUMBER: 40,943

REFERENCE/DOCKET NUMBER: 5940.US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-938-3137

TELEFAX: 847-938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 90 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: protein

DESCRIPTION: internal

FRAGMENT TYPE: internal

US-09-132-154-4

Query Match 84.6%; Score 430; DB 3; Length 90;

Best Local Similarity 82.4%; Pred. No. 9.6e-42;

Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSSTFTPTNKAGLEKXKNCNPDG 60
DB 6 EEDCMFGNGKGYRGKATVTGTPCODMAQEPHRSSTFTPTNPAAGLEKXKNCNPDG 65
QY 61 INGPWCYTNNPRKLFYCDIPICAS 85
DB 66 VGGPWCYTNNPRKLYDYCDVPQCA 90

RESULT 6
US-09-131-995-7
Sequence 7, Application US/09131995
Patent No. 5972896

GENERAL INFORMATION:

APPLICANT: Davidson, Donald J.

TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/131,995

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/832,087

FILING DATE: 03-APR-1997

APPLICATION NUMBER: 08/643,219

FILING DATE: 06-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Casuto, Dianne

REGISTRATION NUMBER: 40,943

REFERENCE/DOCKET NUMBER: 5940.US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-938-3137

TELEFAX: 847-938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 93 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: protein

DESCRIPTION: internal

FRAGMENT TYPE: internal

US-09-131-995-7

Query Match 84.6%; Score 430; DB 2; Length 93;

Best Local Similarity 82.4%; Pred. No. 9.9e-42;

Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EDDCMFGNGKGYRGKATVTGTPCOEWAQEPHRSSTFTPTNKAGLEKXKNCNPDG 60
DB 6 EEDCMFGNGKGYRGKATVTGTPCODMAQEPHRSSTFTPTNPAAGLEKXKNCNPDG 65
QY 61 INGPWCYTNNPRKLFYCDIPICAS 85
DB 66 VGGPWCYTNNPRKLYDYCDVPQCA 90

RESULT 7

US-08-832-087B-7
Sequence 7, Application US/08832087B
Patent No. 5981484

GENERAL INFORMATION:

APPLICANT: Davidson, Donald J.

TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PaateSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932.087B
FILING DATE: 03-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623 *
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: internal
FRAGMENT TYPE: internal
US-08-932-087B-7

[illegible]

[illegible]

APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: internal
FRAGMENT TYPE: internal
US-09-132-154-6

Query Match 84.6%; Score 430; DB 3; Length 98;
Best Local Similarity 82.4%; Pred. No. 1,1e-41;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EDDCMFGNGKGYRGKKAATVTGTGTCQEWAAQEPHRSSTFIPGTNKWAGLEKNYCRNPDD 60
Db 11 EDDCMFGNGKGYRGKKAATVTGTGTCQEWAAQEPHRSSTFIPGTNKWAGLEKNYCRNPDD 70
Qy 61 INGPWCYTNMPKRLFDYCDIPLCAS 85
Db 71 VGGPWCYTNMPKRLYDYCDVPCAA 95

RESULT 15
US-09-131-995-2

Sequence 2, Application US/09131995
Patent No. 5972896
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 101 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: internal
FRAGMENT TYPE: internal
US-09-131-995-2

Query Match 84.6%; Score 430; DB 2; Length 101;
Best Local Similarity 82.4%; Pred. No. 1,1e-41;
Matches 70; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EDDCMFGNGKGYRGKKAATVTGTGTCQEWAAQEPHRSSTFIPGTNKWAGLEKNYCRNPDD 60
Db 17 EDDCMFGNGKGYRGKKAATVTGTGTCQEWAAQEPHRSSTFIPGTNKWAGLEKNYCRNPDD 76
Qy 61 INGPWCYTNMPKRLFDYCDIPLCAS 85
Db 77 VGGPWCYTNMPKRLYDYCDVPCAA 101

Search completed: January 12, 2004, 17:27:16
Job time : 13.2857 secs

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